Compilation of small ribosomal subunit RNA sequences

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INTRODUCTION

Table 1 lists data on 455 small ribosomal subunit RNA (further abbreviated as srRNA) sequences (references 1–452) that have been published or submitted to the EMBL or GenBank nucleotide sequence libraries and that are presently stored in aligned form in our data base. The number identifying each sequence in the first column of Table 1 corresponds with the literature reference. If two or more closely related species share the same sequence, they bear the same number, followed by a different lower case character, and the common sequence is listed only once in our alignment. The set of 452 different sequences consists of 97 eukaryotic cytoplasmic, 19 archaebacterial, 276 eubacterial, 16 plastidial, and 44 mitochondrial srRNAs. It comprises all sequences that to our knowledge had been published or were available from the sequence library file servers as of December 1, 1990, and that are either complete or cover a minimum of about 70% of the complete sequence.

Partial sequences are included because some of the methods now frequently used for srRNA sequencing preclude the determination of the structure at one or both of the termini. One such method consists of reverse transcription of the srRNA by means of primers complementary to conserved areas in the primary structure (453). In this case the 3'-terminal sequence cannot be found. Another approach (55, 328) involves amplification of the rDNA by means of the polymerase chain reaction (454), using primers binding to conserved areas near the termini, but within the sequence coding for the mature small subunit RNA. In this case both terminal sequences remain unknown. Both methods allow to establish a continuous sequence covering more than 95% of the structure, provided that a sufficient number of primers complementary to internal conserved areas is used. Some authors (e.g. 455), however, use a more limited set of primers and publish sequences that are not only partial but also discontinuous.

Establishing a criterion on how large a fraction of a sequence should be known in order for it to be listed in the compilation is less straightforward than it would seem at first sight. Indeed, if nucleotides are missing, be it at the termini or internally, the chain length of the complete srRNA remains unknown, hence the percentage of the sequence that has been determined. Therefore, a criterion of completeness was established with reference to the *Escherichia coli* srRNA sequence, according to the following principle. If a sequence is partial, i.e. it does not reach the termini and/or consists of a number of discontinuous segments, the nucleotides in the *E. coli* sequence homologous to the beginning and the end of each segment are determined. In order for an srRNA sequence to be listed in Table 1, the sequenced segments should correspond to segments in the *E. coli* sequence amounting to a combined length of at least 70% of the complete *E. coli* srRNA. For this computation, rows of nucleotides listed as 'N' are considered as undetermined, i.e. as gaps separating known sequence segments. Since we have started to apply this principle rather recently, it remains possible that a number of sequences that satisfy the criterion are absent from the compilation. We intend to correct any omissions in the future.

In the previous compilation (456), which listed 275 sequences, an alignment for an excerpt of 60 sequences was printed. Due to the large increase of the data set, and the limited space allotted to the compilation, this is no longer possible. However, the complete sequence alignment can be obtained in computer-readable form as specified below. Knowledge of the srRNA secondary structure model, which is largely based on comparative evidence, is essential for the alignment process. This is because not only sequence similarities, but also the boundaries of double- and single stranded areas, guide the alignment. Therefore, the secondary structure model adopted is described below and illustrated with a generalized structure and models for a set of specific srRNAs belonging to different structural types.

SECONDARY STRUCTURE MODEL

Prokaryotic and eukaryotic modelsFig. 1 shows the prokaryotic srRNA secondary structure model, which applies to srRNAs from archaebacterial, eubacterial, plastidial, and mitochondrial ribosomes. The model of Fig. 2 applies to eukaryotic cytoplasmic srRNAs. We define two separate models, even though they have many helices in common, because in certain areas, especially the one labeled V4 in Figures 1 and 2, the structure seems to be essentially different in eukaryotes as compared to bacteria and organelles. In the latter case (Fig. 1), the structure separating helix 21 from helix 22 usually consists of a single hairpin, whereas in eukaryotes (Fig. 2) it comprises up to 9 helices, and none of these shows an obvious homology to the single hairpin in prokaryotes. In other words, transformation of the prokaryotic into the eukaryotic model seems to require deletion of one structure and insertion of an unrelated one. On the other hand, all bacterial and organelle structures can be derived from the general structure of Fig. 1 by mere deletion of appropriate helices, and all eukaryotic structures can be derived similarly from the general structure of Fig. 2.

Helix numbering system

Helices are given a different number if separated by a multibranched loop (e.g. helices 9 and 10), by a pseudoknot loop (e.g. helices 1 and 2), or by a single stranded area that does not

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form a loop (e.g. helices 2 and 30). 'Universal' helices are defined as those that are present in all hitherto known structures of archaebacterial, eubacterial and plastidial srRNAs. They are also present in all eukaryotic srRNAs except that of the microsporidian *Vairimorpha necatrix*, which lacks three of them. They are not universally present, however, in mitochondrial srRNAs, where they can be deleted to various extents. Indeed, the mitochondrial srRNAs are extremely variable in size and structure, ranging from a chain of about 600 nucleotides folded into 25 helices in flagellates, to a chain of about 2000 nucleotides folded into 53 helices in plants. It therefore seems impractical to base a numbering system on the minimal number of helices present in the smallest type of mitochondrial srRNA, and preferable to base it on the helices common to srRNAs of eukaryotes, bacteria, and plastids. The 48 universal helices that can be distinguished according to this definition are given a single number corresponding to the order of occurrence of their 5′-proximal strand when the sequence is scanned starting from the 5′-terminus. Additional helices specific to the prokaryotic model (Fig. 1) are given a composite number of the form Pa−b, where a is the number of the preceding universal helix and b sequentially numbers all helices inserted between universal helices a and a+1. Helices specific to eukaryotic srRNAs are similarly numbered Ea−b. It should be realized that the numbering system is not necessarily definitive since future insights into srRNA secondary structure most probably will reveal the existence of additional P- and E-helices, and possibly of universal helices as well.

Changes with respect to previous models

With respect to the previous sequence compilation (456), two changes have been made to the eukaryotic model (Fig. 2). The interaction previously considered as helix 10 has been rejected because it is not supported by compensating substitutions in the alignment, and the helix previously labeled E10-1 is now considered as helix 10. Hence the old helices E10-2 and E10-3 are renumbered as E10-1 and E10-2. In addition, helix 26 has been lengthened at the expense of helix 20 and the latter is now considered to result from a different interaction than previously proposed. Both aforementioned changes bring our model closer to the one advocated by Gutell and coworkers (457). There subsists one essential difference with the latter model, which concerns the area situated between helices 3 and 5, and constituted by helices 4, 16, 17, 18, and 19. The two models are compared by means of the local structure in yeast srRNA in Fig. 3. Although neither of the alternative structures for helix 4 is hitherto supported by the observation of compensating substitutions, we prefer the topology of Fig. 3b because it is congruent with the topology in prokaryotic srRNAs, illustrated in Fig. 3c with the local structure of *Escherichia coli* srRNA. Contrary to Gutell et al. (457), we propose a tentative secondary structure for the area situated between helices 21 and 22, the derivation of which has been previously published (458). The structure of helix E21-6 belonging to this area has been changed with respect to the previous compilation.

Variable and conserved areas

In Figures 1 and 2, structurally conserved areas are drawn in bold lines, whereas structurally variable areas, labeled V1 to V9, are drawn in thin lines. In general, variability applies to both primary and secondary structure, i.e. alignment areas rich in substitutions are also rich in insertions and deletions, the latter resulting in helices being reduced or extended in length in one species with respect to another. An exception is helix P21-1, indicated as variable in Fig. 1. Though showing many substitutions, it has a constant length, at least among bacteria and plastids. In several variable areas, long insertions present in a limited number of species result in the presence of extra hairpins, drawn in broken lines in Figures 1 and 2. Conversely, deletions may result in the absence of one or more hairpins in certain species.

Subtypes of srRNA secondary structure

As mentioned above, mitochondrial srRNAs show extreme variability in chain length. This coincides with the presence of some of the extra hairpins indicated in Fig. 1, and with deletion, not only of prokaryote-specific, but even universal helices. The helix occupancy in the secondary structure models for srRNAs from archaebacteria, eubacteria, and different types of mitochondria is summarized in Table 2. Among eukaryotic srRNAs, all but one of those hitherto examined share the presence of universal helices 1 to 48, but insertions and deletions of eukaryote-specific helices are observed in areas V2, V4, and V8. Table 3 gives the helix occupancy for those eukaryotic srRNAs that show helix deletions or insertions with respect to the majority of known structures.

Figures 4 to 16 are secondary structure models for a set of srRNAs chosen to illustrate various structural types. *Escherichia coli* srRNA (Fig. 4) obeys the general prokaryotic model, as do all eubacterial and plastidial srRNAs. Archaebacterial srRNAs (Fig. 5) are very similar but lack helices P35-1 and P35-2. Mitochondrial srRNAs possessing supernumerary helices (Fig. 6 to 8) are found in fungi, plants and in the green alga *Prototheca wickerhamii*. Examples of mitochondrial srRNAs with a reduced set of helices are found in the green alga *Chlamydomonas reinhardtii* (Fig. 9) and in the metazoa (Figures 10 and 11). The structure is reduced to its simplest form in flagellate mitochondria, exemplified in Fig. 12 with *Trypanosoma brucei* mitochondrial srRNA. These molecules seem to miss the entire set of adjacent helices 31−45. The model should be considered as tentative, however, since flagellate mitochondrial srRNA sequences, being rich in A and U, are very monotonous and there is no consensus on an optimal alignment with other sequences (450, 451). Yeast cytoplasmic srRNA (Fig. 13) obeys the general eukaryotic model. Examples of eukaryotic srRNAs with extra helices are those of *Drosophila melanogaster* (Fig. 14) and *Euglena gracilis* (Fig. 15), whereas *Vairimorpha necatrix* srRNA (Fig. 16) misses the complete areas V2 and V4.

The structures proposed for the variable areas remain tentative in cases where large inserts occur in a small number of known structures. Examples are the extended helix 18 in yeast mitochondrial srRNA (Fig. 6), the extra helices P41-1 to P41-3 in *Zea mays* mitochondrial srRNA (Fig. 7), the extended helix 41 in *Drosophila melanogaster* cytoplasmic srRNA (Fig. 14), and the extra helix E21-9 in *Euglena gracilis* srRNA (Fig. 15). Each of these can probably be replaced by numerous alternative hypothetical structures showing different internal- and bulge loops or containing additional branching points. The data available at present are insufficient for such local extensions of the model to be supported by the observation of compensating substitutions.

COMPLETENESS, ACCURACY AND AVAILABILITY OF THE DATA

We attempt to align all sequences satisfying the degree of completeness defined in the introduction that are published in journals or available from the GenBank and EMBL nucleotide

sequence libraries. To this end, the EMBL library file server is scanned weekly for new sequences, which are obtained by electronic mail. After alignment and indication of the boundaries of secondary structure elements by means of appropriate programs and editing, newly introduced sequences are scanned for errors by comparison with the original record. Mentions of omitted sequences or errors in the data set will be appreciated.

The srRNA sequences will be available on floppy disks, readable on microcomputers operating under MS-DOS, in the following three formats.

1) The sequences, listed one by one, written continuously without the gaps required for alignment and without indication of secondary structure elements.
2) The sequences, listed one by one, but with nucleotide symbols interspersed with the gaps necessary for alignment. In this file, each sequence covers 4231 positions, which is the present length of the complete alignment.
3) The sequences, listed in the form of an alignment with indication of secondary structure elements. The alignment is divided into 43 pages each comprising 100 positions containing a nucleotide or gap. These positions alternate with extra positions that are either empty or contain a symbol indicating the beginning or end of a secondary structure element. This file, in conjunction with the data in Tables 2 and 3, defines the secondary structure model that we postulate for each sequence. It can be viewed using a text editor or printed by means of a wide carriage (15 inch) matrix printer using condensed print. Printing of the complete alignment requires about 300 pages of 15 inch wide paper.

The number of formatted floppy disks that should be sent in order to obtain the data base in each of these formats is listed in Table 4.

ACKNOWLEDGEMENTS

This work was supported in part by the Incentive Program for Fundamental Research in the Life Sciences of the Belgian Office for Science Policy Programming (grant BIO/03), and in part by the Fund for Medical Scientific Research. P.D.R. holds a scholarship of the Institute for Scientific Research in Agriculture and Industry, J.N. has held a similar scholarship until September 1990.

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Table 1. List of srRNA sequences.

No. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)	Remark
	EUKARYOTES								
1	Homo sapiens 1		Chordata (Ph.)	Mammalia (Cl.)	1869		X03205		i
2	Homo sapiens 2		Chordata (Ph.)	Mammalia (Cl.)	1868		M10098		
3	Homo sapiens 3		Chordata (Ph.)	Mammalia (Cl.)	1870		K03432		
4	Mus musculus		Chordata (Ph.)	Mammalia (Cl.)	1869		X00686		
5	Rattus norvegicus 1	Male Sprague-Dawley, liver	Chordata (Ph.)	Mammalia (Cl.)	1870		M11188		
6	Rattus norvegicus 2	Male Sprague-Dawley, liver	Chordata (Ph.)	Mammalia (Cl.)	1874		X01117		
8	Oryctolagus cuniculus	Reticulocytes	Chordata (Ph.)	Mammalia (Cl.)	1863		X06778		j
9	Xenopus borealis		Chordata (Ph.)	Amphibia (Cl.)	1825				i
10	Xenopus laevis		Chordata (Ph.)	Amphibia (Cl.)	1825		X02995		i
11	Tenebrio molitor	Larvae	Arthropoda (Ph.)	Insecta (Cl.)	1921		X07801		
12	Drosophila melanogaster		Arthropoda (Ph.)	Insecta (Cl.)	1995		M21017		
13	Eurypelma californica	Whole organism	Arthropoda (Ph.)	Arachnida (Cl.)	1814		X13457		
14	Artemia salina	Cysts	Arthropoda (Ph.)	Crustacea (Cl.)	1810		X01723		
15	Argulus nobilis		Arthropoda (Ph.)	Crustacea (Cl.)	(1668)	86.1	M27187		
16	Porocephalus crotali		Arthropoda (Ph.)	Pentastomida (Cl.)	(1662)	85.9	M29931		
17	Caenorhabditis elegans		Nematoda (Ph.)	Secernentea (Cl.)	1760		X03680		
18	Placopecten magellanicus	Strain isolate Placo-1, adductor tissue	Mollusca (Ph.)	Bivalvia (Cl.)	1815		X53899		
19	Anemonia sulcata		Cnidaria (Ph.)	Anthozoa (Cl.)	1799		X53498		
20	Oryza sativa		Magnoliophyta (Div.)	Liliopsida (Cl.)	1812		X00755		
21	Zea mays	Cultivar Black Mexican, leaves	Magnoliophyta (Div.)	Liliopsida (Cl.)	1809		K02202		
22	Lycopersicon esculentum		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1800		X51576		
23	Glycine max	Variety Wayne lambda-SR1	Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1807		X02623		
24	Sinapis alba	Adult stage, bud tissue	Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1804		X17062		
25	Arabidopsis thaliana	Variety Co 10	Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1804		X16077		
26	Fragaria ananassa	Strain genotype 8343-6	Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1804		X15590		
27	Zamia pumila	Leaves	Pinophyta (Div.)	Cycadopsida (Cl.)	1813				
28	Mucor racemosus		Zygomycotina (Ph.)	Zygomycetes (Cl.)	1831		X54863		
29	Neurospora crassa		Ascomycotina (Ph.)	Pyrenomycetes (Cl.)	1795		X04971		
30	Podospora anserina		Ascomycotina (Ph.)	Pyrenomycetes (Cl.)	1796		X54864		
31	Saccharomyces cerevisiae	Strain A364A	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1798		M27607		
32	Schizosaccharomyces pombe		Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1842		X54866		
33	Kluyveromyces lactis	Strain CBS IFO1267	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1793		X51830		
34	Torulaspora delbrueckii	Strain MUCL M27816	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1797		X53496		
35	Candida albicans	Strain MUCL 29800	Deuteromycotina (Ph.)	Blastomycetes (Cl.)	1788		X53497		
36	Candida glabrata	Strain CBS 138	Deuteromycotina (Ph.)	Blastomycetes (Cl.)	1798		X51831		
37	Candida krusei	Strain MUCL 29849	Deuteromycotina (Ph.)	Blastomycetes (Cl.)	1766		M55528		
38	Candida lusitaniae	Strain MUCL 29855	Deuteromycotina (Ph.)	Blastomycetes (Cl.)	1759		M55526		
39	Candida tropicalis	Strain MUCL 30002	Deuteromycotina (Ph.)	Blastomycetes (Cl.)	1785		M55527		
40	Leucosporidium scottii	Strain MUCL 28629	Basidiomycotina (Ph.)		1803		X53499		
41	Pneumocystis carinii	Isolate from rat lung			1813		X12708		
42	Chlamydomonas reinhardtii		Chlorobionts (assemblage)	Chlorophyta (Ph.)	1791		M32703		
43	Volvox carteri	Female Strain HK10 (UTEX 1885)	Chlorobionts (assemblage)	Chlorophyta (Ph.)	1788		X53904		
44	Chlorella fusca		Chlorobionts (assemblage)	Chlorophyta (Ph.)	1795				
45	Chlorella kessleri		Chlorobionts (assemblage)	Chlorophyta (Ph.)	(1797)	99.9			
46	Chlorella minutissima		Chlorobionts (assemblage)	Chlorophyta (Ph.)	1795				
47	Chlorella protothecoides		Chlorobionts (assemblage)	Chlorophyta (Ph.)	1831				
48	Chlorella vulgaris	Type strain 211-11b	Chlorobionts (assemblage)	Chlorophyta (Ph.)	1798		X13688	PCR	
49	Scenedesmus obliquus		Chlorobionts (assemblage)	Chlorophyta (Ph.)	(1794)	99.9			
50	Ankistrodesmus stipitatus		Chlorobionts (assemblage)	Chlorophyta (Ph.)	(1792)	99.8			
51	Prototheca wickerhamii		Chlorobionts (assemblage)	Chlorophyta (Ph.)	(1802)	99.9			
52	Nanochlorum eucaryotum		Chlorobionts (assemblage)	Chlorophyta (Ph.)	1796		X06425		
53	Ochromonas danica		Chromobionts (assemblage)	Chrysophyta (Ph.)	1789		M32704		
54	Costaria costata	Sporophytes	Chromobionts (assemblage)	Phaeophyta (Ph.)	(1595)	87.1	X53229		
55	Skeletonema costatum	Culture 18/C, British Columbia	Chromobionts (assemblage)	Bacillariophyta (Ph.)	(1752)	96.2	X52006	PCR	
56	Porphyra umbilicalis		Rhodophytes (assemblage)	Rhodophyta (Ph.)	1770		X53500		
57	Gracilaria lemaneiformis		Rhodophytes (assemblage)	Rhodophyta (Ph.)	(1771)	99.9	X54263		
58	Gracilaria tikvahiae		Rhodophytes (assemblage)	Rhodophyta (Ph.)	1771		M33640		
59	Gracilaria verrucosa		Rhodophytes (assemblage)	Rhodophyta (Ph.)	1771		M33638		
60	Gracilariopsis sp.		Rhodophytes (assemblage)	Rhodophyta (Ph.)	1782		M33639		
61	Blastocladiella emersonii	Strain L17 ATCC 22665	Mastigomycetes (assemblage)	Chytridiomycota (Ph.)	1901		X54264		
62	Achlya bisexualis		Mastigomycetes (assemblage)	Oomycota (Ph.)	1809		M32705		
63	Phytophtora megasperma	Isolate P3114	Mastigomycetes (assemblage)	Oomycota (Ph.)	1827		X54265		
64	Lagenidium giganteum	Strain ATCC 52675	Mastigomycetes (assemblage)	Oomycota (Ph.)	1822		X54266		
65	Euplotes aediculatus		Ciliates (assemblage)	Ciliophora (Ph.)	1882		X03949		
66	Oxytricha nova		Ciliates (assemblage)	Ciliophora (Ph.)	1771		X03948		
67	Stylonychia pustulata		Ciliates (assemblage)	Ciliophora (Ph.)	1771		X03947		
68	Tetrahymena australis	Strain MGO (intron-), ATCC 30831	Ciliates (assemblage)	Ciliophora (Ph.)	1752				
69a	Tetrahymena borealis	Strain UM 731 (intron-)	Ciliates (assemblage)	Ciliophora (Ph.)	1752		M26359		
69b	Tetrahymena canadensis	Strain UM 1215, ATCC 30368	Ciliates (assemblage)	Ciliophora (Ph.)	1752				
70	Tetrahymena capricornis	Strain AU-F1-1 (intron-), ATCC 30291	Ciliates (assemblage)	Ciliophora (Ph.)	1752				
71	Tetrahymena hegewischi	Strain KP7 (intron-), ATCC 30832	Ciliates (assemblage)	Ciliophora (Ph.)	1752				
72	Tetrahymena malaccensis	Strain MP75 (intron+), ATCC 50066	Ciliates (assemblage)	Ciliophora (Ph.)	1753		M26360		
73	Tetrahymena patula	Strain LFF (intron-), ATCC 50064	Ciliates (assemblage)	Ciliophora (Ph.)	1752				
74a	Tetrahymena pigmentosa	Strain UM 1286 (intron-)	Ciliates (assemblage)	Ciliophora (Ph.)	1752		M26358		
74b	Tetrahymena hyperangularis	Strain EN 101, ATCC 30273	Ciliates (assemblage)	Ciliophora (Ph.)	1752				
74c	Tetrahymena nanneyi	Strain XQ5, ATCC 30840	Ciliates (assemblage)	Ciliophora (Ph.)	1752				
75	Tetrahymena pyriformis	Strain GL-C (intron-, a-micronuclear)	Ciliates (assemblage)	Ciliophora (Ph.)	1752				

Table 1. continued

No. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)	Remark
76	Tetrahymena thermophila	Strain A-17682a (intron+), ATTC 30377	Ciliates (assemblage)	Ciliophora (Ph.)	1753		M10932		
77	Tetrahymena tropicalis	Strain TC3 (intron-), ATCC 30352	Ciliates (assemblage)	Ciliophora (Ph.)	1752				
78	Paramecium tetraurelia		Ciliates (assemblage)	Ciliophora (Ph.)	1753		X03772		
79	Prorocentrum micans	Strain LB113614	Dinoflagellates (assemblage)	Peridinea (Ph.)	1801		M14649		
80	Plasmodium berghei 1	Strain NUY2	Sporozoa (assemblage)	Sporozoa (Ph.)	2060				
81	Plasmodium berghei 2		Sporozoa (assemblage)	Sporozoa (Ph.)	2059				
82	Plasmodium falciparum 1		Sporozoa (assemblage)	Sporozoa (Ph.)	2091				
83	Plasmodium falciparum 2		Sporozoa (assemblage)	Sporozoa (Ph.)	2146				
84	Plasmodium lophurae		Sporozoa (assemblage)	Sporozoa (Ph.)	2118		X13706		
85	Plasmodium vivax		Sporozoa (assemblage)	Sporozoa (Ph.)	(1605)	73.7	X13926		
86	Acanthamoeba castellanii		Rhizopods (assemblage)	Amoebozoa (Ph.)	2303		M13435		
87	Naegleria gruberi		Rhizopods (assemblage)	Amoebozoa (Ph.)	2019		M18732		
88	Dictyostelium discoideum	Strain Ax3	Rhizopods (assemblage)	Eumycetozoa (Ph.)	(1872)	99.9	K02641		j
89	Physarum polycephalum	Strain CL	Rhizopods (assemblage)	Eumycetozoa (Ph.)	1964		X13160		
90	Trypanosoma brucei		Euglenozoa (assemblage)	Kinetoplastidea (Ph.)	2251		M12676		
91	Trypanosoma cruzi		Euglenozoa (assemblage)	Kinetoplastidea (Ph.)	2319		M31432		
92	Crithidia fasciculata		Euglenozoa (assemblage)	Kinetoplastidea (Ph.)	2206		X03450		
93	Leishmania donovani	Strain Sudan 1	Euglenozoa (assemblage)	Kinetoplastidea (Ph.)	2205		X07773		
94	Euglena gracilis		Euglenozoa (assemblage)	Euglenophyta (Ph.)	2305		M12677		
95	Vairimorpha necatrix		Microsporidia (assemblage)	Microsporidia (Ph.)	1244		Y00266		
96	Giardia intestinalis	Trophozoite, cell line BRIS/83/HEPU/106	Polymastigotes (assemblage)		(1452)	99.9	X52949		
97	Giardia lamblia	Strain Portland 1	Polymastigotes (assemblage)		1451				
	ARCHAEBACTERIA								
98	Halobacterium cutirubrum		Halobacteria		1472		K02971		
99	Halobacterium halobium	Strain RI	Halobacteria		1473		M38280		
100	Halobacterium volcanii		Halobacteria		1472		K00421		
101	Halococcus morrhuae	Strain ATCC 17082	Halobacteria		1475		X00662		
102	Methanospirillum hungatei	Strain JF1	Methanomicrobium group		(1438)	98.3			
103	Methanothrix soehngenii		Methanomicrobium group		1471		X16932		
104	Methanococcus vannielii	Strain DSM 1224	Methanococcus group		1466		M36507		
105	Methanobacterium formicicum	Strain DSM 1312	Methanobacter group		1476		M36508		
106	Methanobacterium thermoautotrophicum	Strain Marburg	Methanobacter group		1482		X15364		
107	Methanothermus fervidus		Methanobacter group		1481		M32222		
108	Thermococcus celer	Strain DSM 2476	Thermococcus group		1486				
109	Thermoplasma acidophilum	Strain 122-1B2	Thermoplasma		1471		M38637		
110	Thermofilum pendens	Strain Hvv3, DSM 2475	Extreme thermophiles		1509		X14835		
111	Desulfurococcus mobilis		Extreme thermophiles		1495		M36474		
112	Pyrodictium occultum	Strain PL-19 DSM 2709	Extreme thermophiles		(1494)	99.8	M21087		
113	Sulfolobus shibatae		Extreme thermophiles		1495		M32504		
114	Sulfolobus solfataricus	Strain P1	Extreme thermophiles		1493		X03235		j
115	Thermoproteus tenax		Extreme thermophiles		1504		M35966		
116	Archaeoglobus fulgidus	Strain VC-16	Uncertain affiliation		1492		X05567		
	EUBACTERIA								
117	Agrobacterium tumefaciens	Strain DSM 30105	Proteobacteria (Cl.)	Alpha group (Scl.)	1489		M11223		
118	Brucella abortus	Strain 11/19	Proteobacteria (Cl.)	Alpha group (Scl.)	(1429)	96.5	X13695	RT	
119	Ehrlichia risticii	Strain ATCC VR986	Proteobacteria (Cl.)	Alpha group (Scl.)	(1498)	100.0	M21290		
120	Hyphomicrobium vulgare	Strain MC-750	Proteobacteria (Cl.)	Alpha group (Scl.)	(1383)	93.5	X53182	RT	
121	Caulobacter crescentus	Strain CB2	Proteobacteria (Cl.)	Alpha group (Scl.)	(1259)	84.7	X52281		
122	Rickettsia prowazekii		Proteobacteria (Cl.)	Alpha group (Scl.)	(1508)	100.0	M21789		
123	Rickettsia rickettsii	Strain ATCC VR891	Proteobacteria (Cl.)	Alpha group (Scl.)	(1432)	95.5	M21293	RT	
124	Rickettsia typhi		Proteobacteria (Cl.)	Alpha group (Scl.)	(1349)	88.3	M20499	RT	
125	Rochalimaea quintana	Strain Fuller	Proteobacteria (Cl.)	Alpha group (Scl.)	1491		M11927		
126	Methylobacterium extorquens	Strain AM1	Proteobacteria (Cl.)	Alpha group (Scl.)	(1338)	87.8	M29027	RT	
127	Methylobacterium organophilum	Strain XX	Proteobacteria (Cl.)	Alpha group (Scl.)	(1282)	85.8	M29028	RT	
128	Methylocystis parvus	Strain OBBP	Proteobacteria (Cl.)	Alpha group (Scl.)	(1294)	86.9	M29026	RT	
129	Methylosinus trichosporium	Strain OB3b	Proteobacteria (Cl.)	Alpha group (Scl.)	(1435)	95.7	M29024	RT	
130	Methylosporovibrio methanica	Strain 81Z	Proteobacteria (Cl.)	Alpha group (Scl.)	(1284)	86.7	M29025	RT	
131	Rhodospirillum rubrum		Proteobacteria (Cl.)	Alpha group (Scl.)	(1402)	94.2	M32020		
132	Rhodopseudomonas acidophila		Proteobacteria (Cl.)	Alpha group (Scl.)	(1461)	97.6	M34128		
133	Rhodopseudomonas marina		Proteobacteria (Cl.)	Alpha group (Scl.)	(1389)	94.7	M27534		
134	Rhodobacter capsulatus		Proteobacteria (Cl.)	Alpha group (Scl.)	(1389)	93.4	M34129		
135	Rhodomicrobium vannielii		Proteobacteria (Cl.)	Alpha group (Scl.)	(1419)	95.2	M34127		
136	Rhodocyclus purpureus		Proteobacteria (Cl.)	Alpha group (Scl.)	(1472)	95.6	M34132		
137	Alcaligenes eutrophus		Proteobacteria (Cl.)	Beta group (Scl.)	(1502)	97.7	M32021		
138	Alcaligenes faecalis	Strain ATCC 8750	Proteobacteria (Cl.)	Beta group (Scl.)	(1458)	94.8	M22508	RT	
139	Alcaligenes xylosoxidans	Strain ATCC 15173	Proteobacteria (Cl.)	Beta group (Scl.)	(1450)	94.5	M22509	RT	
140	Chromobacterium fluviatile	Strain ATCC 33051	Proteobacteria (Cl.)	Beta group (Scl.)	(1435)	93.5	M22511	RT	
141	Chromobacterium violaceum	Strain ATCC 12472	Proteobacteria (Cl.)	Beta group (Scl.)	(1464)	95.1	M22510	RT	
142	Eikenella corrodens 1	Strain ATCC 23834	Proteobacteria (Cl.)	Beta group (Scl.)	(1450)	94.0	M22512	RT	
143	Eikenella corrodens 2	Strain FDC 373	Proteobacteria (Cl.)	Beta group (Scl.)	(1428)	92.4	M22513	RT	
144	Eikenella corrodens 3	Strain FDC 558	Proteobacteria (Cl.)	Beta group (Scl.)	(1406)	90.4	M22514	RT	
145	Eikenella corrodens 4	Strain FDC 1073	Proteobacteria (Cl.)	Beta group (Scl.)	(1438)	93.1	M22515	RT	
146	Kingella denitrificans	Strain ATCC 33394	Proteobacteria (Cl.)	Beta group (Scl.)	(1468)	95.4		RT	
147	Kingella kingae	Strain ATCC 23330	Proteobacteria (Cl.)	Beta group (Scl.)	(1470)	95.5	M22517	RT	
148	Neisseria gonorrhoeae 1	Strain NCTC 8375	Proteobacteria (Cl.)	Beta group (Scl.)	1544		X07714		
149	Neisseria gonorrhoeae 2		Proteobacteria (Cl.)	Beta group (Scl.)	(1456)	94.5	M34130		

Table 1. continued

No. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)	Remark
150	Acinetobacter calcoaceticus		Proteobacteria (Cl.)	Beta group (SCl.)	(1509)	98.1	M34139		
151	Vitreoscilla stercoraria	Strain VT1	Proteobacteria (Cl.)	Beta group (SCl.)	(1481)	96.0	M22519	RT	
152	Methylophilus methylotrophus	Strain AS1	Proteobacteria (Cl.)	Beta group (SCl.)	(1497)	96.9	M29021	RT	
153	Pseudomonas cepacia	Strain ATCC 25416	Proteobacteria (Cl.)	Beta group (SCl.)	(1449)	94.5	M22518	RT	
154	Pseudomonas testosteroni	Strain ATCC 11996	Proteobacteria (Cl.)	Beta group (SCl.)	1536		M11224		
155	Pseudomonas aeruginosa 1	Strain ATCC 11996	Proteobacteria (Cl.)	Gamma group (SCl.)	1537		X06684		
156	Pseudomonas aeruginosa 2		Proteobacteria (Cl.)	Gamma group (SCl.)	(1489)	96.7	M34133		
157	Acyrthosyphon pisum symbiont P		Proteobacteria (Cl.)	Gamma group (SCl.)	1547		M27039		
158	Acyrthosyphon pisum symbiont S		Proteobacteria (Cl.)	Gamma group (SCl.)	1542		M27040		
159	Chromatium vinosum	Strain ATCC 17899	Proteobacteria (Cl.)	Gamma group (SCl.)	(1491)	97.3	M26629	RT	
160	Coxiella burnetii	Strain Q177	Proteobacteria (Cl.)	Gamma group (SCl.)	(1476)	95.5	M21291	RT	
161	Ectothiorhodospira halophila		Proteobacteria (Cl.)	Gamma group (SCl.)	(1454)	93.7	M26630		
162	Escherichia coli	Operon rrnB	Proteobacteria (Cl.)	Gamma group (SCl.)	1542		V00348		k
163	Proteus vulgaris 1		Proteobacteria (Cl.)	Gamma group (SCl.)	1544		J01874		j
164	Proteus vulgaris 2	Strain IFAM 1731	Proteobacteria (Cl.)	Gamma group (SCl.)	1544		X07652		
165	Ruminobacter amylophilus	Strain DSM 1361	Proteobacteria (Cl.)	Gamma group (SCl.)	1539				
166	Wolbachia persica	Strain ATCC VR331	Proteobacteria (Cl.)	Gamma group (SCl.)	(1462)	95.0	M21292	RT	
167	Xylella fastidiosa		Proteobacteria (Cl.)	Gamma group (SCl.)	(1477)	95.5	M26601		
168	Vibrio anguillarum	Strain ATCC 12964 (T)	Proteobacteria (Cl.)	Gamma group (SCl.)	(1503)	97.4	X16895		
169	Xenorhabdus nematophilus		Proteobacteria (Cl.)	Gamma group (SCl.)	(1238)	79.0	X53188		
170	Desulfosarcina variabilis 1		Proteobacteria (Cl.)	Delta group (SCl.)	(1502)	95.9	M66320		
171	Desulfosarcina variabilis 2	Strain DSM 2060	Proteobacteria (Cl.)	Delta group (SCl.)	(1509)	96.0	M34407	RT	
172	Desulfovibrio africanus		Proteobacteria (Cl.)	Delta group (SCl.)	(1244)	78.2	M37315	RT	
173	Desulfovibrio baarsii	Strain DSM 2075	Proteobacteria (Cl.)	Delta group (SCl.)	(1348)	85.8	M34403	RT	
174	Desulfovibrio baculatus		Proteobacteria (Cl.)	Delta group (SCl.)	(1286)	81.1	M37311	RT	
175	Desulfovibrio desulfuricans 1	Strain ATCC 27774	Proteobacteria (Cl.)	Delta group (SCl.)	(1550)	99.9	M34113		
176	Desulfovibrio desulfuricans 2		Proteobacteria (Cl.)	Delta group (SCl.)	(1273)	81.0	M37316	RT	
177	Desulfovibrio desulfuricans 3		Proteobacteria (Cl.)	Delta group (SCl.)	(1287)	81.6	M37312	RT	
178	Desulfovibrio gigas	Strain ATCC 19364	Proteobacteria (Cl.)	Delta group (SCl.)	(1278)	80.7	M34400	RT	
179	Desulfovibrio salexigens	Strain ATCC 14822	Proteobacteria (Cl.)	Delta group (SCl.)	(1311)	82.9	M34401	RT	
180	Desulfovibrio sapovorans	Strain ATCC 33892	Proteobacteria (Cl.)	Delta group (SCl.)	(1348)	85.8	M34402	RT	
181	Desulfovibrio vulgaris	Strain DSM 644	Proteobacteria (Cl.)	Delta group (SCl.)	(1310)	83.3	M34399	RT	
182	Desulfobacter curvatus	Strain DSM 3379	Proteobacteria (Cl.)	Delta group (SCl.)	(1362)	86.7	M34413	RT	
183	Desulfobacter hydrogenophilus	Strain DSM 3380	Proteobacteria (Cl.)	Delta group (SCl.)	(1374)	87.4	M34412	RT	
184	Desulfobacter lactus	Strain DSM 3381	Proteobacteria (Cl.)	Delta group (SCl.)	(1218)	76.5	M34414	RT	
185	Desulfobacter postgatei		Proteobacteria (Cl.)	Delta group (SCl.)	(1501)	96.2	M26633		
186	Desulfobacter sp. 1	Strain DSM 2035	Proteobacteria (Cl.)	Delta group (SCl.)	(1449)	92.0	M34416	RT	
187	Desulfobacter sp. 2	Strain DSM 2057	Proteobacteria (Cl.)	Delta group (SCl.)	(1369)	87.0	M34415	RT	
188	Desulfomonas pigra	Strain ATCC 29098	Proteobacteria (Cl.)	Delta group (SCl.)	(1232)	80.4	M34404	RT	
189	Desulfococcus multivorans	Strain ATCC 33890	Proteobacteria (Cl.)	Delta group (SCl.)	(1351)	86.3	M34405	RT	
190	Desulfobulbus propionicus	Strain ATCC 33891	Proteobacteria (Cl.)	Delta group (SCl.)	(1297)	82.0	M34410	RT	
191	Desulfobulbus sp.	Strain DSM 2058	Proteobacteria (Cl.)	Delta group (SCl.)	(1254)	78.6	M34411	RT	
192	Desulfobacterium autotrophicum	Strain DSM 3382	Proteobacteria (Cl.)	Delta group (SCl.)	(1329)	84.3	M34409	RT	
193	Desulfobacterium niacini	Strain DSM 2650	Proteobacteria (Cl.)	Delta group (SCl.)	(1182)	73.0	M34406	RT	
194	Desulfobacterium vacuolatum	Strain DSM 3385	Proteobacteria (Cl.)	Delta group (SCl.)	(1363)	86.1	M34408	RT	
195	Spirillum volutans		Proteobacteria (Cl.)	Delta group (SCl.)	(1469)	95.5	M34131		
196	Helicobacter felis		Proteobacteria (Cl.)	Delta group (SCl.)	(1377)	91.3	M35047		
197	Helicobacter mustelae		Proteobacteria (Cl.)	Delta group (SCl.)	(1417)	94.2	M35048		
198	Bdellovibrio stolpii		Proteobacteria (Cl.)	Delta group (SCl.)	(1461)	93.6	M34125		
199	Desulfomonile tiedjei		Proteobacteria (Cl.)	Delta group (SCl.)	(1469)	93.8	M26635		
200	Desulfuromonas acetoxidans	Strain DSM 684	Proteobacteria (Cl.)	Delta group (SCl.)	(1494)	95.3	M26634	RT	
201	Myxococcus xanthus	Strain MD207	Proteobacteria (Cl.)	Delta group (SCl.)	(1539)	99.9	M34114		
202	Wolinella succinogenes	Strain ATCC 29453	Proteobacteria (Cl.)	Uncertain affiliation	(1449)	96.1		RT	
203	Hirschia baltica	Strain IFAM 1418	Proteobacteria (Cl.)	Uncertain affiliation	(1379)	94.9	X52909		
204	Desulfotomaculum orientis	Strain NCIMB 8382	Firmicuta (Ph.)	Low G+C	(1232)	76.5	M34417	RT	
205	Desulfotomaculum ruminis	Strain NCIMB 8452	Firmicuta (Ph.)	Low G+C	(1324)	85.8	M34418	RT	
206	Acholeplasma entomophilum	Strain TAC, ATCC 43706	Firmicuta (Ph.)	Low G+C	(1438)	93.1	M23931	RT	
207	Acholeplasma laidlawii	Strain JA1	Firmicuta (Ph.)	Low G+C	(1508)	100.0	M23932	RT	
208	Acholeplasma modicum	Strain PG49, ATCC 29102	Firmicuta (Ph.)	Low G+C	(1468)	95.9	M23933	RT	
209	Anaeroplasma abactoclasticum	Strain 6-1, ATCC 27879	Firmicuta (Ph.)	Low G+C	(1449)	96.4	M25050	RT	
210	Anaeroplasma bactoclasticum	Strain JR, ATCC 27112	Firmicuta (Ph.)	Low G+C	(1425)	95.8	M25049	RT	
211	Anaeroplasma varium	Strain A-2, ATCC 43167	Firmicuta (Ph.)	Low G+C	(1428)	96.2	M23934	RT	
212	Asteroleplasma anaerobium	Strain 161, ATCC 27880	Firmicuta (Ph.)	Low G+C	(1466)	95.7	M22351	RT	
213	Bacillus subtilis	Operon rrnB	Firmicuta (Ph.)	Low G+C	1550		K00637		
214	Clostridium aminovalericum		Firmicuta (Ph.)	Low G+C	(1526)	98.1	M23929	RT	
215	Clostridium barkeri		Firmicuta (Ph.)	Low G+C	(1507)	98.5	M23927	RT	
216	Clostridium innocuum	Strain B-3, ATCC 14501	Firmicuta (Ph.)	Low G+C	(1539)	99.9	M23732	RT	
217	Clostridium pasteurianum		Firmicuta (Ph.)	Low G+C	(1483)	97.9	M23930	RT	
218	Clostridium ramosum	Strain 113-I, ATCC 25582	Firmicuta (Ph.)	Low G+C	(1513)	98.6	M23731	RT	
219	Clostridium sticklandii		Firmicuta (Ph.)	Low G+C	(1467)	95.9	M26494	RT	
220	Carnobacterium divergens	Strain NCDO 2763 (T)	Firmicuta (Ph.)	Low G+C	(1466)	93.6	X54270	RT	
221	Carnobacterium gallinarum	Strain NCFB 2766 (T)	Firmicuta (Ph.)	Low G+C	(1465)	93.7	X54269	RT	
222	Carnobacterium mobile	Strain NCFB 2765 (T)	Firmicuta (Ph.)	Low G+C	(1345)	86.0	X54271	RT	
223	Carnobacterium piscicola	Strain NCDO 2762 (T)	Firmicuta (Ph.)	Low G+C	(1467)	94.1	X54268	RT	
224	Erysipelothrix rhusiopathiae	Strain alpha-P15, ATCC 19414	Firmicuta (Ph.)	Low G+C	(1482)	96.2	M23728	RT	
225	Leuconostoc cremoris	Strain DSM 20346	Firmicuta (Ph.)	Low G+C	(1488)	95.6	M23034	RT	
226	Leuconostoc lactis	Strain DSM 20202	Firmicuta (Ph.)	Low G+C	(1470)	94.6	M23031	RT	
227	Leuconostoc mesenteroides	Strain DSM 20343	Firmicuta (Ph.)	Low G+C	(1530)	89.1	M23035	RT	

Table 1. continued

No. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)	Remark
228	Leuconostoc oenos	Strain DSM 20252	Firmicuta (Ph.)	Low G+C	(1488)	95.0	M35820	RT	
229	Leuconostoc paramesenteroides		Firmicuta (Ph.)	Low G+C	(1511)	95.5	M23033	RT	
230	Lactobacillus casei		Firmicuta (Ph.)	Low G+C	(1549)	98.1	M23928	RT	
231	Lactobacillus catenaforme	Strain 1871, ATCC 25536	Firmicuta (Ph.)	Low G+C	(1508)	96.5	M23729	RT	
232	Lactobacillus confusus 1	Strain NCDO 5186	Firmicuta (Ph.)	Low G+C	(1457)	92.3	X52567	RT	
233	Lactobacillus confusus 2	Strain DSM 20196	Firmicuta (Ph.)	Low G+C	(1511)	95.7	M23036	RT	
234	Lactobacillus halotolerans	Strain DSM 20190	Firmicuta (Ph.)	Low G+C	(1502)	94.8	M23037	RT	
235	Lactobacillus kandleri 1	Strain NCDO 2753	Firmicuta (Ph.)	Low G+C	(1477)	93.6	X52570	RT	
236	Lactobacillus kandleri 2	Strain DSM 20593	Firmicuta (Ph.)	Low G+C	(1510)	95.5	M23038		
237	Lactobacillus minor 1	Strain NCDO 1973	Firmicuta (Ph.)	Low G+C	(1475)	93.6	X52569	RT	
238	Lactobacillus minor 2	Strain DSM 20014	Firmicuta (Ph.)	Low G+C	(1511)	95.6	M23039	RT	
239	Lactobacillus viridescens 1	Strain NCDO 1655	Firmicuta (Ph.)	Low G+C	(1467)	93.1	X52568	RT	
240	Lactobacillus viridescens 2	Strain ATCC 12706	Firmicuta (Ph.)	Low G+C	(1553)	97.7	M23040	RT	
241	Lactobacillus vitulinus	Strain 185, ATCC 27783	Firmicuta (Ph.)	Low G+C	(1463)	95.4	M23727	RT	
242	Arthrobacter globiformis		Firmicuta (Ph.)	Low G+C	1531		M23411	RT	
243	Lactococcus garviae	Strain NCDO 2156	Firmicuta (Ph.)	Low G+C	(1437)	93.1	X54262	RT	
244	Lactococcus lactis	Strain NCDO 2118	Firmicuta (Ph.)	Low G+C	(1420)	91.7	X54260	RT	
245	Lactococcus piscium	Strain NCFB 2778	Firmicuta (Ph.)	Low G+C	(1430)	91.2	X53905	RT	
246	Lactococcus plantarum	Strain NCDO 1869	Firmicuta (Ph.)	Low G+C	(1423)	92.0	X54259	RT	
247	Lactococcus raffinolactis	Strain NCDO 617	Firmicuta (Ph.)	Low G+C	(1439)	92.4	X54261	RT	
248	Mycoplasma agalactiae	Strain PG2, NCTC 10123	Firmicuta (Ph.)	Low G+C	(1455)	95.7	M24290	RT	
249	Mycoplasma arginini	Strain G230, ATCC 23838	Firmicuta (Ph.)	Low G+C	(1421)	91.9	M24579	RT	
250	Mycoplasma arthritidis	Strain PG6, ATCC 19611	Firmicuta (Ph.)	Low G+C	(1527)	96.0	M24580	RT	
251	Mycoplasma bovigenitalium	Strain PG11, ATCC 19852	Firmicuta (Ph.)	Low G+C	(1454)	95.7	M24291	RT	
252	Mycoplasma californicum	Strain ST-6, ATCC 33461	Firmicuta (Ph.)	Low G+C	(1486)	96.5	M24582	RT	
253	Mycoplasma capricolum		Firmicuta (Ph.)	Low G+C	1521		X00921		
254	Mycoplasma ellychniae	Strain ELCN-1, ATCC 43707	Firmicuta (Ph.)	Low G+C	(1443)	92.9	M24292	RT	
255	Mycoplasma fermentans	Strain PG18, ATCC 19989	Firmicuta (Ph.)	Low G+C	(1447)	95.5	M24289	RT	
256	Mycoplasma gallisepticum		Firmicuta (Ph.)	Low G+C	1519		M22441		
257	Mycoplasma hominis	Strain PG21, ATCC 23114	Firmicuta (Ph.)	Low G+C	(1406)	92.2	M24473	RT	
258	Mycoplasma hyopneumoniae	Strain ATCC 27719	Firmicuta (Ph.)	Low G+C	1537		Y00149		
259	Mycoplasma hyorhinis	Strain ATCC 17981	Firmicuta (Ph.)	Low G+C	(1411)	90.7	M24658	RT	
260	Mycoplasma iowae	Strain 695, ATCC 33552	Firmicuta (Ph.)	Low G+C	(1441)	94.9	M24293	RT	
261	Mycoplasma lipophilum	Strain MaBy, ATCC 27104	Firmicuta (Ph.)	Low G+C	(1466)	95.1	M24581	RT	
262	Mycoplasma mobile	Strain 1634, ATCC 43663	Firmicuta (Ph.)	Low G+C	(1460)	96.2	M24480	RT	
263	Mycoplasma muris	Strain RIII4, ATCC 33757	Firmicuta (Ph.)	Low G+C	(1456)	95.8	M23939	RT	
264	Mycoplasma mycoides	Strain UM30847	Firmicuta (Ph.)	Low G+C	(1421)	91.9	M23943	RT	
265	Mycoplasma neurolyticum	Strain type A, ATCC 19988	Firmicuta (Ph.)	Low G+C	(1474)	95.8	M23944	RT	
266	Mycoplasma orale	Strain CH19299, ATCC 23714	Firmicuta (Ph.)	Low G+C	(1447)	95.1	M24659	RT	
267	Mycoplasma pirum	Strain 70-159, ATCC 25960	Firmicuta (Ph.)	Low G+C	(1464)	96.5	M23940	RT	
268	Mycoplasma pneumoniae	Strain FH, ATCC 15531	Firmicuta (Ph.)	Low G+C	(1463)	96.4	M29061	RT	
269	Mycoplasma pulmonis	Strain PG34, ATCC 19612	Firmicuta (Ph.)	Low G+C	(1426)	92.5	M23941	RT	
270	Mycoplasma putrefaciens	Strain KS-1, ATCC 15718	Firmicuta (Ph.)	Low G+C	(1416)	92.0	M23938	RT	
271	Mycoplasma salivarium	Strain PG20, ATCC 23064	Firmicuta (Ph.)	Low G+C	(1419)	92.0	M24661	RT	
272	Mycoplasma sualvi	Strain Mayfield B, ATCC 33004	Firmicuta (Ph.)	Low G+C	(1443)	92.2	M23936	RT	
273	Mycoplasma sp. 1	Strain 831-C4, ATCC 49193	Firmicuta (Ph.)	Low G+C	(1420)	91.6	M24479	RT	
274	Mycoplasma sp. 2	Strain M1, ATCC 49191	Firmicuta (Ph.)	Low G+C	(1448)	94.2	M24478	RT	
275	Mycoplasma sp. 3	Strain PG 50, Operon rrnA	Firmicuta (Ph.)	Low G+C	1523		M10588	RT	
276	Oenothera hookeri MLO		Firmicuta (Ph.)	Low G+C	1535				
277	Spiroplasma apis	Strain B-31, ATCC 33834	Firmicuta (Ph.)	Low G+C	(1411)	92.0	M23937	RT	
278	Spiroplasma citri	Strain ATCC 27556	Firmicuta (Ph.)	Low G+C	(1503)	98.2	M23942	RT	
279	Spiroplasma group II	Strain DW1, ATCC 43153	Firmicuta (Ph.)	Low G+C	(1457)	96.0	M24483	RT	
280	Spiroplasma group VI	Strain Y32, ATCC 33835	Firmicuta (Ph.)	Low G+C	(1426)	92.5	M24477	RT	
281	Spiroplasma group VII	Strain MQ-1, ATCC 33825	Firmicuta (Ph.)	Low G+C	(1401)	91.4	M24481	RT	
282	Spiroplasma group IX	Strain CN-5, ATCC 33827	Firmicuta (Ph.)	Low G+C	(1390)	89.4	M24474	RT	
283	Spiroplasma group XII	Strain DM-1, ATCC 43210	Firmicuta (Ph.)	Low G+C	(1418)	92.9	M24482	RT	
284	Spiroplasma group XXIII	Strain TG-1, ATCC 43525	Firmicuta (Ph.)	Low G+C	(1459)	95.7	M24475	RT	
285	Spiroplasma mirum	Strain SMCA, ATCC 29335	Firmicuta (Ph.)	Low G+C	(1413)	91.8	M24662	RT	
286	Spiroplasma tiawanense group XXII	Strain CT-1, ATCC 43302	Firmicuta (Ph.)	Low G+C	(1415)	92.0	M24476	RT	
287	Streptococcus pleomorphus	Strain 60B, ATCC 29734	Firmicuta (Ph.)	Low G+C	(1557)	95.2	M23730	RT	
288	Streptococcus parasanguis	Strain 85-81	Firmicuta (Ph.)	Low G+C	(1443)	92.9	X53652	RT	
289	Streptococcus parauberis	Strain NCDO 651	Firmicuta (Ph.)	Low G+C	(1417)	91.4		RT	
290	Streptococcus sanguis	Strain NCTC 7863	Firmicuta (Ph.)	Low G+C	(1429)	92.0	X53653	RT	
291	Streptococcus uberis	Strain NCDO 643	Firmicuta (Ph.)	Low G+C	(1438)	92.9		RT	
292	Ureaplasma urealyticum	Strain 960, NCTC 10177	Firmicuta (Ph.)	Low G+C	(1462)	96.4	M23935	RT	
293	Vagococcus fluvialis	Strain NCDO 2497	Firmicuta (Ph.)	Low G+C	(1439)	92.3	X54258	RT	
294	Vagococcus salmoninarum	Strain NCFB 27777 (T)	Firmicuta (Ph.)	Low G+C	(1460)	93.3	X54272	RT	
295	Peptococcus niger		Firmicuta (Ph.)	Low G+C	(1404)	89.5	X55797		
296	Megasphaera elsdenii		Firmicuta (Ph.)	High G+C	(1539)	97.9	M26493	RT	
297	Selenomonas lacticifex	Strain DSM 20757	Firmicuta (Ph.)	High G+C	(1457)	92.7		RT	
298	Selenomonas ruminantium	Strain DSM 2872	Firmicuta (Ph.)	High G+C	(1457)	92.4		RT	
299	Selenomonas sputigena	Strain ATCC 35185	Firmicuta (Ph.)	High G+C	(1497)	96.4		RT	
300	Zymophilus paucivorans	Strain DSM 20756	Firmicuta (Ph.)	High G+C	(1455)	92.3		RT	
301	Pectinatus cerevisiiphilus	Strain ATCC 29359	Firmicuta (Ph.)	High G+C	(1433)	91.2		RT	
302	Pectinatus frisigensis	Strain ATCC 33332	Firmicuta (Ph.)	High G+C	(1442)	91.8		RT	
303	Actinomyces bovis 1		Firmicuta (Ph.)	High G+C	(1344)	87.3	M33909		
304	Actinomyces bovis 2	Strain DSM 43014	Firmicuta (Ph.)	High G+C	(1344)	87.1	X53224		
305	Actinomyces israeli	Strain DSM 43020	Firmicuta (Ph.)	High G+C	(1340)	87.7	X53228	RT	

Table 1. continued

No. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)	Remark
306	Actinomyces naeslundii 1		Firmicuta (Ph.)	High G+C	(1349)	85.7	M33911		
307	Actinomyces naeslundii 2	Strain DSM 43013	Firmicuta (Ph.)	High G+C	(1352)	86.1	X53226	RT	
308	Actinomyces odontolyticus 1		Firmicuta (Ph.)	High G+C	(1327)	85.5	M33910	RT	
309	Actinomyces odontolyticus 2	Strain DSM 43331	Firmicuta (Ph.)	High G+C	(1337)	86.1	X53227	RT	
310	Actinomyces pyogenes	Strain ATCC 19411	Firmicuta (Ph.)	High G+C	(1350)	87.7	M29552	RT	
311	Actinomyces viscosus	Strain DSM 43027	Firmicuta (Ph.)	High G+C	(1426)	92.2	X53225	RT	
312	Aeromicrobium erythreus		Firmicuta (Ph.)	High G+C	(1430)	94.6	M37200		
313	Nocardia asteroides	Strain DSM 43005	Firmicuta (Ph.)	High G+C	(1343)	87.7	X53205		
314	Faenia rectivirgula	Strain ATCC 33515 (T)	Firmicuta (Ph.)	High G+C	(1263)	81.8	X53194		
315	Terrabacter tumescens	Strain NCIB 8914	Firmicuta (Ph.)	High G+C	(1376)	90.2	X53215	RT	
316	Sphaerobacter thermophilus	Strain 6022 DSM 20745 (T)	Firmicuta (Ph.)	High G+C	(1138)	74.3	X53210		
317	Mycobacterium asiaticum	Strain ATCC 25276	Firmicuta (Ph.)	High G+C	(1362)	89.0	M29556	RT	
318	Mycobacterium aurum	Strain ATCC 23366	Firmicuta (Ph.)	High G+C	(1331)	87.7	M29558	RT	
319	Mycobacterium avium 1	Serovar 4	Firmicuta (Ph.)	High G+C	(1350)	88.0	M29572	RT	
320	Mycobacterium avium 2	Serovar 1	Firmicuta (Ph.)	High G+C	(1351)	87.7	M29573	RT	
321	Mycobacterium bovis	Strain BCG	Firmicuta (Ph.)	High G+C	1535				
322	Mycobacterium chelonei	Strain ATCC 19977	Firmicuta (Ph.)	High G+C	(1345)	88.5	M29559	RT	
323	Mycobacterium chitae	Strain ATCC 19627	Firmicuta (Ph.)	High G+C	(1348)	88.7	M29560	RT	
324	Mycobacterium cookii	Strain ATCC 49103 (T) = NZ2	Firmicuta (Ph.)	High G+C	(1445)	94.3	X53896	RT	
325	Mycobacterium fallax	Strain ATCC 35219	Firmicuta (Ph.)	High G+C	(1346)	87.2	M29562	RT	
326	Mycobacterium flavescens	Strain ATCC 14474	Firmicuta (Ph.)	High G+C	(1352)	88.8	M29561	RT	
327	Mycobacterium gordonae	Strain ATCC 14470	Firmicuta (Ph.)	High G+C	(1366)	89.2	M29563	RT	
328	Mycobacterium kansasii	Strain DSM 43224	Firmicuta (Ph.)	High G+C	(1460)	95.3	X15916	RT	
329	Mycobacterium leprae		Firmicuta (Ph.)	High G+C	1548		X53999		
330	Mycobacterium neoaurum	Strain ATCC 25795	Firmicuta (Ph.)	High G+C	(1346)	88.8	M29564	RT	
331	Mycobacterium nonchromogenicum	Strain ATCC 19530	Firmicuta (Ph.)	High G+C	(1367)	88.4	M29565	RT	
332	Mycobacterium paratuberculosis		Firmicuta (Ph.)	High G+C	(1362)	89.0	M29569	RT	
333	Mycobacterium phlei	Strain ATCC 11758	Firmicuta (Ph.)	High G+C	(1354)	88.7	M29566	RT	
334	Mycobacterium senegalense	Strain ATCC 35796	Firmicuta (Ph.)	High G+C	(1350)	88.9	M29567	RT	
335	Mycobacterium terrae	Strain ATCC 15755	Firmicuta (Ph.)	High G+C	(1360)	88.7	M29568	RT	
336	Mycobacterium thermoresistible	Strain ATCC 19527	Firmicuta (Ph.)	High G+C	(1352)	88.7	M29570	RT	
337	Mycobacterium triviale	Strain ATCC 23292	Firmicuta (Ph.)	High G+C	(1336)	87.7	M29571	RT	
338	Mycobacterium sp. 1 (Chromogen)	Bovine feces	Firmicuta (Ph.)	High G+C	(1349)	88.1	M29554	RT	
339	Mycobacterium sp. 2	Strain 3937	Firmicuta (Ph.)	High G+C	(1323)	85.9	M29555	RT	
340	Nocardioides albus	Strain DSM 43109	Firmicuta (Ph.)	High G+C	(1425)	93.3	X53211	RT	
341	Nocardioides fastidiosa	Strain NCIB 12713 (T)	Firmicuta (Ph.)	High G+C	(1417)	93.6	X53189		
342	Nocardioides jensenii	Strain DSM 29641	Firmicuta (Ph.)	High G+C	(1419)	93.0	X53214	RT	
343	Nocardioides luteus	Strain NCIB 11455	Firmicuta (Ph.)	High G+C	(1433)	94.2	X53212	RT	
344	Nocardioides simplex 1	Strain NCIB 8929	Firmicuta (Ph.)	High G+C	(1415)	92.6		RT	
345	Nocardioides simplex 2	Strain NCIB 8929 (T)	Firmicuta (Ph.)	High G+C	(1373)	90.6	X53213	RT	
346	Rhodococcus erythropolis	Strain DSM 43188	Firmicuta (Ph.)	High G+C	(1340)	87.5	X53203		
347	Rhodococcus equi	Equine lung	Firmicuta (Ph.)	High G+C	(1351)	88.8	M29574	RT	
348	Rhodococcus fascians	Strain DSM 20131	Firmicuta (Ph.)	High G+C	(1301)	85.0	X53204		
349	Propionibacterium acidi-propionici	Strain DSM 20272	Firmicuta (Ph.)	High G+C	(1324)	85.8	X53221	RT	
350	Propionibacterium acnes	Strain DSM 1897	Firmicuta (Ph.)	High G+C	(1336)	87.0	X53218	RT	
351	Propionibacterium freudenreichii	Strain DSM 20271	Firmicuta (Ph.)	High G+C	(1443)	94.4	X53217	RT	
352	Propionibacterium jensenii	Strain DSM 20535	Firmicuta (Ph.)	High G+C	(1333)	86.9	X53219	RT	
353	Propionibacterium thoenii	Strain DSM 20276	Firmicuta (Ph.)	High G+C	(1437)	93.8	X53220	RT	
354	Streptomyces ambofaciens	Operon rrnD	Firmicuta (Ph.)	High G+C	1528		M27245		
355	Streptomyces coelicolor	Strain A3 (2) M145, Operon rrnD	Firmicuta (Ph.)	High G+C	(1527)	99.9	Y00411		
356	Streptomyces lividans	Strain TK21, Operon rrnB	Firmicuta (Ph.)	High G+C	1531		Y00484		
357	Tsukamurella paurometabolum	Strain DSM 20162, NCTC 10741	Firmicuta (Ph.)	High G+C	(1315)	86.2		RT	
358	Gordona terrae	Strain DSM 43249	Firmicuta (Ph.)	High G+C	(1326)	86.4	X53202		
359	Mobiluncus curtisii	Strain ATCC 35421	Firmicuta (Ph.)	High G+C	(1344)	86.7	X53186	RT	
360	Amycolatopsis azurae	Strain NRRL 11412	Firmicuta (Ph.)	High G+C	(1277)	83.6	X53199		
361	Amycolatopsis fastidiosa	Strain ATCC 31181	Firmicuta (Ph.)	High G+C	(1306)	85.0	X53200		
362	Amycolatopsis methanolica		Firmicuta (Ph.)	High G+C	(1418)	93.5		RT	
363	Amycolata autotrophica	Strain DSM 43210	Firmicuta (Ph.)	High G+C	(1302)	85.0	X54288		
364	Saccharomonospora viridis	Strain ATCC 15386	Firmicuta (Ph.)	High G+C	(1354)	88.4	X54286		
365	Saccharopolyspora erythraea	Strain NRRL 2338	Firmicuta (Ph.)	High G+C	(1285)	83.5	X53198		
366	Saccharopolyspora hirsuta	Strain ATCC 27875 (T)	Firmicuta (Ph.)	High G+C	(1337)	86.5	X53196		
367	Saccharopolyspora hordei	Strain A54	Firmicuta (Ph.)	High G+C	(1306)	84.2	X53197		
368	Actinopolyspora halophila	Strain ATCC 279	Firmicuta (Ph.)	High G+C	(1301)	84.0	X54287		
369	Pseudonocardia thermophila	Strain ATCC 19285 (T)	Firmicuta (Ph.)	High G+C	(1275)	82.6	X53195		
370	Corynebacterium polymorphus	Strain NCDO 2097	Firmicuta (Ph.)	High G+C	(1429)	93.6			
371	Corynebacterium renale	Strain ATCC 19412	Firmicuta (Ph.)	High G+C	(1354)	88.5	M29553	RT	
372	Corynebacterium variabilis	Strain NCIB 9455 (T), NCDO 2097 (T)	Firmicuta (Ph.)	High G+C	(1432)	93.6	X53185	RT	
373	Heliobacterium chlorum		Firmicuta (Ph.)	Photosynthetic org.	(1512)	99.1	M11212		
374	Leptospira interrogans	Serovar canicola Strain Moulton	Spirochetes & rel. (Ph.)	Leptospira subdivision	1508		X17547		
375	Thermus thermophilus	Strain HB8	Radioresistant micrococci & rel. (Ph.)	Thermophiles group	1515		X07998		
376	Deinococcus radiodurans	Strain UWO 298	Radioresistant micrococci & rel. (Ph.)	Deinococcus group	1502		M21413		
377	Bacteroides fragilis	Strain ATCC 25285	Bacteroides, Flavobact., Cytophaga (Ph.)	Bacteroides	1533		M11656		
378	Cytophaga heparina	Strain IFO 12017, ATCC 13125	Bacteroides, Flavobact., Cytophaga (Ph.)	Flavobacterium group	(1521)	99.5	M11657		
379	Chlamydia psittaci	Strain 6BC	Chlamydiae (Ph.)		1552		M13769		
380	Chloroflexus aurantiacus	Strain J10FL	Green non sulfur bacteria & rel. (Ph.)	Chloroflexus group	(1425)	95.7	M34116	RT	
381	Herpetosiphon aurantiacus	Strain ATCC 23779	Green non sulfur bacteria & rel. (Ph.)	Chloroflexus group	(1430)	95.9	M34117	RT	
382	Thermomicrobium roseum	Strain ATCC 27502	Green non sulfur bacteria & rel. (Ph.)	Thermomicrobium group	(1523)	99.5	M34115		

Table 1. continued

No. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)	Re-mark
383	Clathrochloris sulfurica	Strain 1	Green sulfur bacteria (Ph.)		(1288)	83.9	X53184	RT	
384	Chlorobium limicola		Green sulfur bacteria (Ph.)		(1482)	98.5	M31769	RT	
385	Anacystis nidulans	Strain 6301 (Berkeley)	Cyanobacteria (Ph.)		1487		X03538		
386	Planctomyces staleyi		Planctomyces & rel. (Ph.)		(1521)	99.7	M34126		
387	Thermotoga maritima	Strain MSB 8, DSM 3109	Thermophilic eubacteria		(1561)	99.9			
388	Arhodomonas oleiferhydrans		Uncertain affiliation		(1464)	95.1	M26631		
389	Syntrophomonas wolfei		Uncertain affiliation		(1409)	88.8	M26492	RT	
390	Syntrophospora bryantii		Uncertain affiliation		(1465)	93.2	M26491	RT	
391	Unknown 6	Clone SAR6	Uncertain affiliation		(1470)	99.8	X52169	PCR	
392	Unknown 7	Clone SAR7	Uncertain affiliation		(1473)	99.7	X52171	PCR	
	PLASTIDS								
393	Zea mays		Magnoliophyta (Div.)	Liliopsida (Cl.)	1491		Z00028		
394	Oryza sativa		Magnoliophyta (Div.)	Liliopsida (Cl.)	1491		X15901		
395	Nicotiana tabacum 1	Variety Bright Yellow 4	Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1486		V00165		
396	Nicotiana tabacum 2	Variety Bright Yellow 4	Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1489		Z00044		
397	Glycine max		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1470		X06428		
398	Marchantia polymorpha		Bryophyta (Div.)	Marchantiopsida (Cl.)	1496		X04465		
399	Chlamydomonas eugametos		Chlorobionts (assemblage)	Chlorophyta (Ph.)	1481				
400	Chlamydomonas moewusii		Chlorobionts (assemblage)	Chlorophyta (Ph.)	1481				
401	Chlamydomonas reinhardtii		Chlorobionts (assemblage)	Chlorophyta (Ph.)	(1477)	99.2	X03269		
402	Chlorella ellipsoidea	Strain IAM-C87	Chlorobionts (assemblage)	Chlorophyta (Ph.)	1584				
403	Chlorella vulgaris	Strain 211-11b	Chlorobionts (assemblage)	Chlorophyta (Ph.)	(1494)	99.8	X16579		
404	Pylaiella littoralis	Clone pPLiE4	Chromobionts (assemblage)	Phaeophyta (Ph.)	1505		X14873		
405	Ochromonas danica	Strain 933-7	Chromobionts (assemblage)	Chrysophyta (Ph.)	(1256)	81.9	X53183	RT	
406	Cyanidium caldarium	Strain 14-1-1	Rhodophytes (assemblage)	Rhodophyta (Ph.)	1492		X52985		
407	Euglena gracilis	Strain Z	Euglenozoa (assemblage)	Euglenophyta (Ph.)	1496		V00159		
408	Astasia longa	Strain CCAP 1204-17a	Euglenozoa (assemblage)	Euglenophyta (Ph.)	1520		X14386		
	MITOCHONDRIA								
409	Homo sapiens	Placenta	Chordata (Ph.)	Mammalia (Cl.)	954		V00710		
410	Pan paniscus	Frozen tissue	Chordata (Ph.)	Mammalia (Cl.)	950				
411	Pan troglodytes	Cultured cells	Chordata (Ph.)	Mammalia (Cl.)	949				
412	Gorilla gorilla	Frozen tissue	Chordata (Ph.)	Mammalia (Cl.)	949				
413	Pongo pigmaeus	Frozen tissue	Chordata (Ph.)	Mammalia (Cl.)	952				
414	Mus musculus	L-cell, C2-1 line	Chordata (Ph.)	Mammalia (Cl.)	956				
415	Rattus norvegicus 1	Liver	Chordata (Ph.)	Mammalia (Cl.)	953		V00680		
416	Rattus norvegicus 2	Variant A	Chordata (Ph.)	Mammalia (Cl.)	957		X14848		
417	Bos taurus	Heart	Chordata (Ph.)	Mammalia (Cl.)	955		V00654		
418	Odocoileus virginianus		Chordata (Ph.)	Mammalia (Cl.)	953		M35874		
419	Cervus unicolor		Chordata (Ph.)	Mammalia (Cl.)	955		M35875		
420	Hydropotes inermis		Chordata (Ph.)	Mammalia (Cl.)	957		M35876		
421	Muntiacus reevesi		Chordata (Ph.)	Mammalia (Cl.)	959		M35877		
422	Gallus gallus	White Leghorn, adult, liver	Chordata (Ph.)	Aves (Cl.)	976		X52392		
423	Rana catesbeiana		Chordata (Ph.)	Amphibia (Cl.)	937		X12841		
424	Xenopus laevis		Chordata (Ph.)	Amphibia (Cl.)	945		M27605		
425	Drosophila virilis	Stock 2375.8, Chile	Arthropoda (Ph.)	Insecta (Cl.)	787				
426	Drosophila yakuba	Stock 2371.6, Ivory coast	Arthropoda (Ph.)	Insecta (Cl.)	789		X03240		
427	Strongylocentrotus purpuratus		Echinodermata (Ph.)	Echinoidea (Cl.)	878		X12631		
428	Paracentrotus lividus	Fresh eggs	Echinodermata (Ph.)	Echinoidea (Cl.)	883		J04815		
429	Zea diploperennis	Seedlings	Magnoliophyta (Div.)	Liliopsida (Cl.)	1968				
430	Zea mays 1		Magnoliophyta (Div.)	Liliopsida (Cl.)	1968		X00794		
431	Zea mays 2		Magnoliophyta (Div.)	Liliopsida (Cl.)	1967		M10248		
432	Triticum aestivum		Magnoliophyta (Div.)	Liliopsida (Cl.)	1955		K01229		
433	Glycine max	Cultivar Williams	Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1990		M16859		
434	Oenothera sp.		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1901				
435	Aspergillus nidulans	Strain paba A1, bi A1	Ascomycotina (Ph.)	Plectomycetes (Cl.)	1554		V00653		
436	Podospora anserina	Race A	Ascomycotina (Ph.)	Pyrenomycetes (Cl.)	1980		X14734		
437	Saccharomyces cerevisiae 1	Strain MH41-7B	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1669		V00702		
438	Saccharomyces cerevisiae 2	Strain D273-10B, wild-type	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1686		V00704		
439	Saccharomyces cerevisiae 3	Strain 777-3A	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1651		X07800		
440	Saccharomyces cerevisiae 4	Strain KL14-4A	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1649		X07799		
441	Schizosaccharomyces pombe		Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1422		X15738		
442	Prototheca wickerhamii	Strain 263-11	Chlorobionts (assemblage)	Chlorophyta (Ph.)	1680		X15435		
443	Chlamydomonas reinhardtii		Chlorobionts (assemblage)	Chlorophyta (Ph.)	1200		M25119		1
444	Tetrahymena pyriformis 1	Strain ST	Ciliates (assemblage)	Ciliophora (Ph.)	1660		X05203		
445	Tetrahymena pyriformis 2	Strain ST	Ciliates (assemblage)	Ciliophora (Ph.)	1669		M12714		
446	Paramecium aurelia	Strain species 4, stock 51	Ciliates (assemblage)	Ciliophora (Ph.)	1688		X15917		
447	Paramecium primaurelia	Stock 513 (Edinburgh)	Ciliates (assemblage)	Ciliophora (Ph.)	1672		K01750		m
448	Paramecium tetraurelia	Stock 51 (Edinburgh)	Ciliates (assemblage)	Ciliophora (Ph.)	(1661)	99.9	K01751		m
449	Trypanosoma brucei	Strain 427	Euglenozoa (assemblage)	Kinetoplastidea (Ph.)	611		V01390		
450	Crithidia fasciculata		Euglenozoa (assemblage)	Kinetoplastidea (Ph.)	612		X02548		
451	Leishmania tarentolae		Euglenozoa (assemblage)	Kinetoplastidea (Ph.)	607				
452	Leptomonas sp.		Euglenozoa (assemblage)	Kinetoplastidea (Ph.)	611		J03814		

Footnotes to Table 1

a) This number corresponds with the literature reference. Identical numbers, followed by a different lower case character, are attributed to srRNAs from related species, or from different strains of the same species, that have the same sequence (e.g. Tetrahymena borealis and Tetrahymena canadensis, no. 69, a and b) In such cases only one sequence is listed in our computer file.

b) When different sequences are determined for various strains or genes of the same organism, the sequences are listed separately and the species name is followed by a number.

c) This column contains the following data, if specified by the authors:

- Strain name for laboratory animals, (cultivated) variety for plants, culture collection and strain number in the case of microorganisms.
- Tissue from which the DNA used for cloning or amplification was extracted in the case of differentiated organisms.
- Ribosomal RNA operon to which belongs the cloned srRNA gene in the case of bacteria.

d) The taxonomic position is described according to the following references: 459 for the metazoa (No. 1 to 19), 460 for the higher plants (No. 20 to 27), and 461 for the higher fungi (No. 28 to 41). The taxonomic position of the remaining eukaryotes is described according to Corliss (462). The archaebacteria are classified according to Woese (463). The classification of the eubacteria is according to Stackebrandt et al. (464) for the Proteobacteria, according to Wayne et al. (465) for the Firmicuta, and according to Woese (463) for the remaining taxa. We have no information yet on the taxonomic position of species 388-392. Taxon designations corresponding to an established taxonomic level are followed by the abbreviation Ph. (Phylum), Div. (Division), Cl. (Class), SCl. (Subclass) and O. (Order).

e) The srRNA termini are located experimentally (e.g. by S1 nuclease mapping) by some authors, but more often deduced by comparison with structures from related species. In case of length heterogeneity the length of the longest variant is listed. A number enclosed in brackets means that the sequence is incomplete and gives the number of sequenced nucleotides. This includes partially identified nucleotides denoted as B, D, H, K, M, R, S, V, W or Y, but not unidentified nucleotides denoted as N.

f) For incomplete sequences, this is the combined length of the corresponding E. coli srRNA segments as a fraction of the total E. coli srRNA length. This may amount to 100% even for an incomplete sequence because a missing segment may be situated in an insertion relative to the E. coli sequence.

g) Accession number in the EMBL and Genbank nucleotide sequence libraries. The accession number for a sequence is the same in both libraries but there can be a delay before a sequence submitted to one library arrives in the other one.

h) RT: the srRNA was sequenced by the dideoxynucleotide method using reverse transcriptase. PCR: amplification of the DNA involved use of polymerase chain reaction. In the remaining cases DNA was amplified by cloning only. Sequencing of amplified DNA was performed in most cases by the dideoxynucleotide method.

i) Complete data on nucleoside modification can be found in the paper reporting this sequence.

j) Partial data on modified nucleosides are mentioned in this paper or other papers cited therein.

k) Complete data on nucleoside modification can be found in (466), but the sequence listed there misses 1 nucleotide and has been corrected in (162).

l) Chlamydomonas reinhardtii mitochondrial srRNA consists of a set of 4 discrete fragments. The corresponding sequences in the rDNA are interspersed with genes coding for tRNAs, large ribosomal subunit RNA fragments, and proteins.

m) The location of the termini is uncertain.

Table 2. Helix occupancy in bacterial, plastidial and mitochondrial srRNAs.

Sequence number (a)	Species (b)	Universal helices (c)																										Prokaryote-specific helices (c)									
																		31 to 34		36 to 38								P 17	P 21		P 35		P 41			P 45	
		6	9	10	11	12	13	14	15	17	18	24	26	27	28	29		35		39	40	41	42	43	44	45		1	1	2	1	2	1	2	3	1	2
98 to 116	Archaebacterial	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	-	-	-	-	-	-	-	-
117 to 392	Eubacterial	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	-	*	*	-	-	-	-	-
393 to 408	Plastidial	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	-	*	*	-	-	-	-	-
	Mitochondrial:																																				
409 to 414	Homo sapiens	*	-	-	-	*	*	-	*	-	-	*	*	-	-	*	*	-	*	*	*	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
415 to 416	Rattus norvegicus	-	-	-	-	*	*	-	*	-	-	*	*	-	-	*	*	-	*	*	*	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
417	Bos taurus	*	-	-	-	*	-	-	*	-	-	*	*	-	-	*	*	-	*	-	*	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
418,421	Odocoileus virginianus	-	-	-	-	*	*	-	*	-	-	*	*	-	-	*	*	-	*	-	*	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
419,420,423	Cervus unicolor	-	-	-	-	*	-	-	*	-	-	*	*	-	-	*	*	-	*	-	*	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
422	Gallus gallus	*	-	-	-	*	*	-	*	-	-	-	*	-	-	*	*	-	*	*	*	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
424	Xenopus laevis	-	-	-	-	*	-	-	-	-	-	*	*	-	-	*	*	-	*	-	*	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
425	Drosophila virilis	*	-	-	-	-	-	-	-	-	-	*	-	-	-	*	*	-	*	*	*	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
426	Drosophila yakuba	*	-	-	-	-	-	-	*	-	-	*	-	-	-	*	*	-	*	*	*	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
427	Strongylocentrotus purpuratus	*	-	-	-	*	*	-	*	-	-	*	-	-	-	*	*	-	*	-	-	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
428	Paracentrotus lividus	-	-	-	-	*	*	-	*	-	-	*	-	-	-	*	*	-	*	-	-	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-
429 to 434	Zea mays	*	*	*	-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	-	*	*	*	*	*	-	-
435	Aspergillus nidulans	*	*	-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	-	-	-	-	-	-	-	-
436	Podospora anserina	*	*	-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	-	(d)	(d)	-	-	-	-	-
437,438	Saccharomyces cerevisiae type 1	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	*	-	-	-	-	-
439,440	Saccharomyces cerevisiae type 2	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	-	*	*	-	-	-	-	-
441	Schizosaccharomyces pombe	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	-	-	-	-	-	-	-	-
442	Prototheca wickerhamii	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	*	*	*	-	-	-	-	-
443	Chlamydomonas reinhardtii	*	-	-	-	*	*	*	*	*	-	*	*	-	-	*	*	*	*	*	*	-	-	*	*	*	-	-	-	-	-	-	-	-	-	*	*
444 to 448	Tetrahymena pyriformis	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	-	*	-	*	*	-	-	-	-	-
449 to 452	Trypanosoma brucei	*	*	*	-	-	*	-	-	*	-	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*	-	-	-	-	-	-	-	-

a) Numbers correspond to those used in Table 1.
b) In the case of mitochondrial srRNAs, this column lists an example of a species where this helix occupancy is found.
c) The presence of a helix is indicated by an asterisk. The complete set of 48 universal helices is present in archaebacterial, eubacterial and plant mitochondrial srRNAs. Those helices that are not listed occur in all hitherto known srRNAs, including those of mitochondria.
d) Podospora anserina mitochondrial srRNA contains an insertion, relative to other sequences, of 164 nucleotides between the 5′ and 3′ strands of helix 35. It is uncertain wether this structure merely extends hairpin 35 or contains additional branching points.

Table 3. Helix occupancy in eukaryotic srRNAs.

Sequence number (a)	Species	Helix (b)												
		E 8	E 10		E 21									E 43
		1	1	2	1	2	3	4	5	6	7	8	9	1
96 to 97	Giardia lamblia	-	-	-	-	-	-	-	*	*	*	*	-	-
95	Vairimorpha necatrix	-	-	-	-	-	-	-	-	-	-	-	-	-
94	Euglena gracilis	*	*	*	*	-	*	*	*	*	*	*	*	*
90 to 93	Trypanosoma brucei	*	*	-	*	-	*	-	*	*	*	*	*	*
87	Naegleria gruberi	-	*	*	*	-	*	*	*	*	*	*	-	*
86	Acanthamoeba castellanii	-	*	-	*	-	*	*	*	*	*	*	-	*
80 to 85	Plasmodium berghei	-	*	-	*	-	*	-	*	*	*	*	-	*
65	Euplotes aediculatus	*	*	-	*	-	*	*	*	*	*	*	-	*
89	Physarum polycephalum	*	*	*	*	-	*	-	*	*	*	*	-	*
12	Drosophila melanogaster	-	*	-	*	*	*	-	*	*	*	*	-	-
	All other eukaryotes	-	*	-	*	-	*	-	*	*	*	*	-	-

a) Numbers correspond to those used in Table 1.
b) The presence of a helix is indicated by an asterisk. Only eukaryotic helices are listed since universal helices are present in all eukaryotic srRNAs, except for Vairimorpha necatrix srRNA, which misses helices 10, 11 and 44.

Table 4. Number of formatted disks to be sent in order to obtain a copy of the database. See text for a description of the different formats.

Disk type		Database format (see text)		
Size	Capacity	Format 1	Format 2	Format 3
5.25"	DSDD (360 Kbytes)	3	7	13
5.25"	DSHD (1.2 Mbytes)	1	2	4
3.5"	DSDD (720 Kbytes)	2	4	7
3.5"	DSHD (1.44 Mbytes)	1	2	4

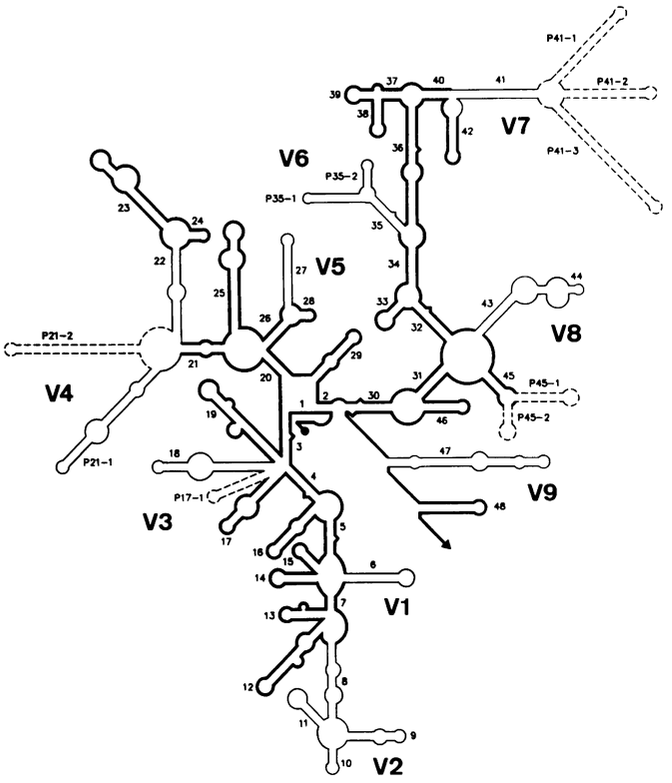


Fig. 1. Secondary structure model for prokaryotic srRNAs.The 5′-terminus is symbolized by a dot, the 3′-terminus by an arrowhead. Helices are numbered in the order of occurrence from 5′- to 3′-terminus. Helices bearing a single number are common to the prokaryotic and eukaryotic (Fig. 2) models. Helices bearing a composite number preceded by P are prokaryote-specific. Areas of relatively conserved primary structure are drawn in bold lines. Nine variable areas labeled V1 to V9 are drawn in thin lines. Helices drawn in broken lines are present exceptionally. See Table 2 for a complete survey of helix occupancy in known structures.

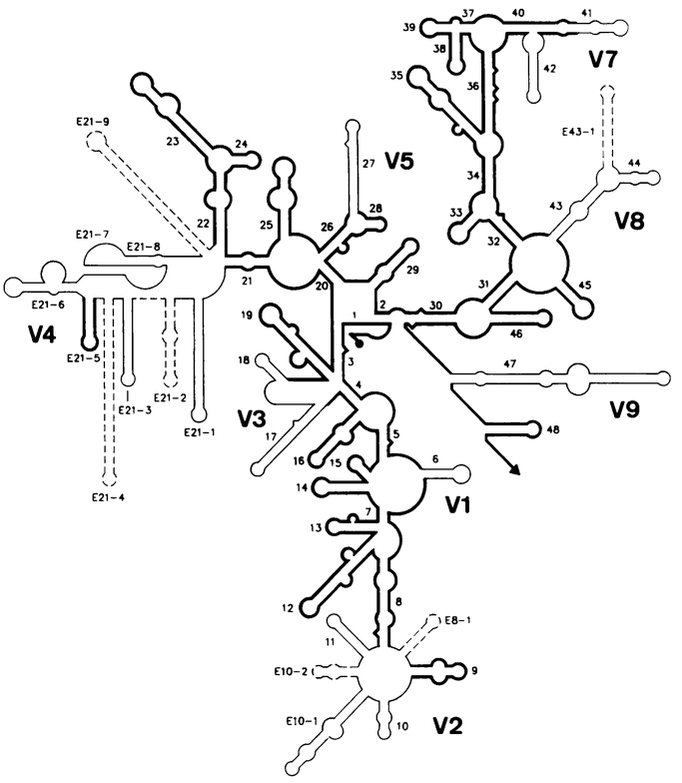


Fig. 2. Secondary structure model for eukaryotic srRNAs.Symbols are as in Fig. 1. Helices bearing a composite number preceded by E are eukaryote-specific. The area corresponding to V6 in Fig. 1 is more conserved among eukaryotic srRNAs. See Table 3 for a complete survey of helix occupancy in known structures.

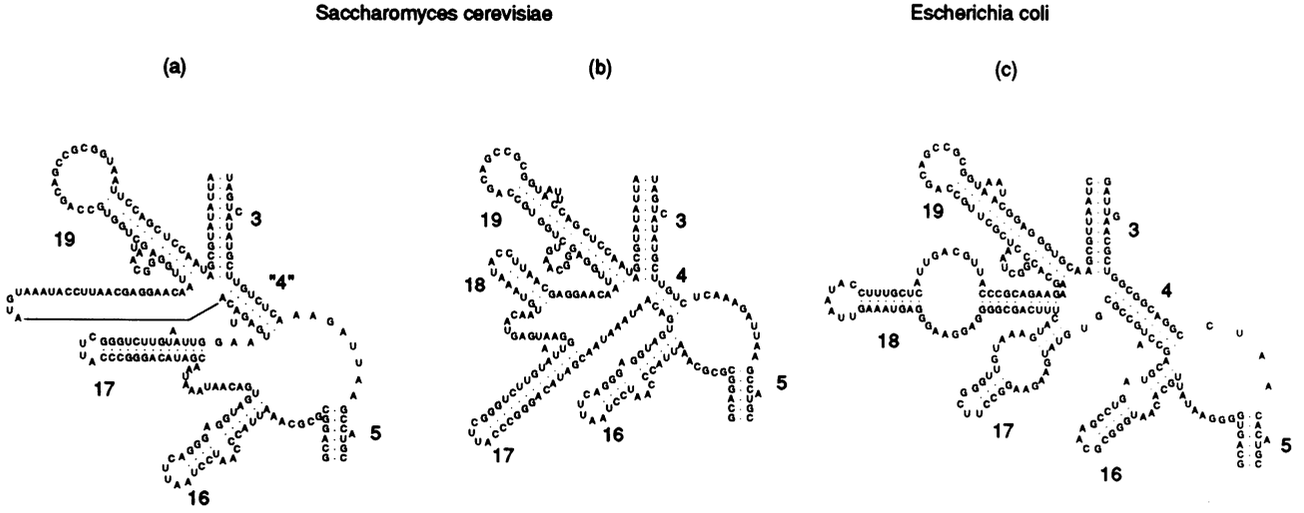


Fig. 3. Comparison of two possible base pairing schemes for the area between helices 3 and 5 in eukaryotic srRNAs.The two structures are illustrated in (a) and (b) with the *Saccharomyces cerevisiae* sequence.(a) Structure according to Gutell et al. (457)
(b) Structure adopted in this paper.
(c) Corresponding structure in *Escherichia coli*.

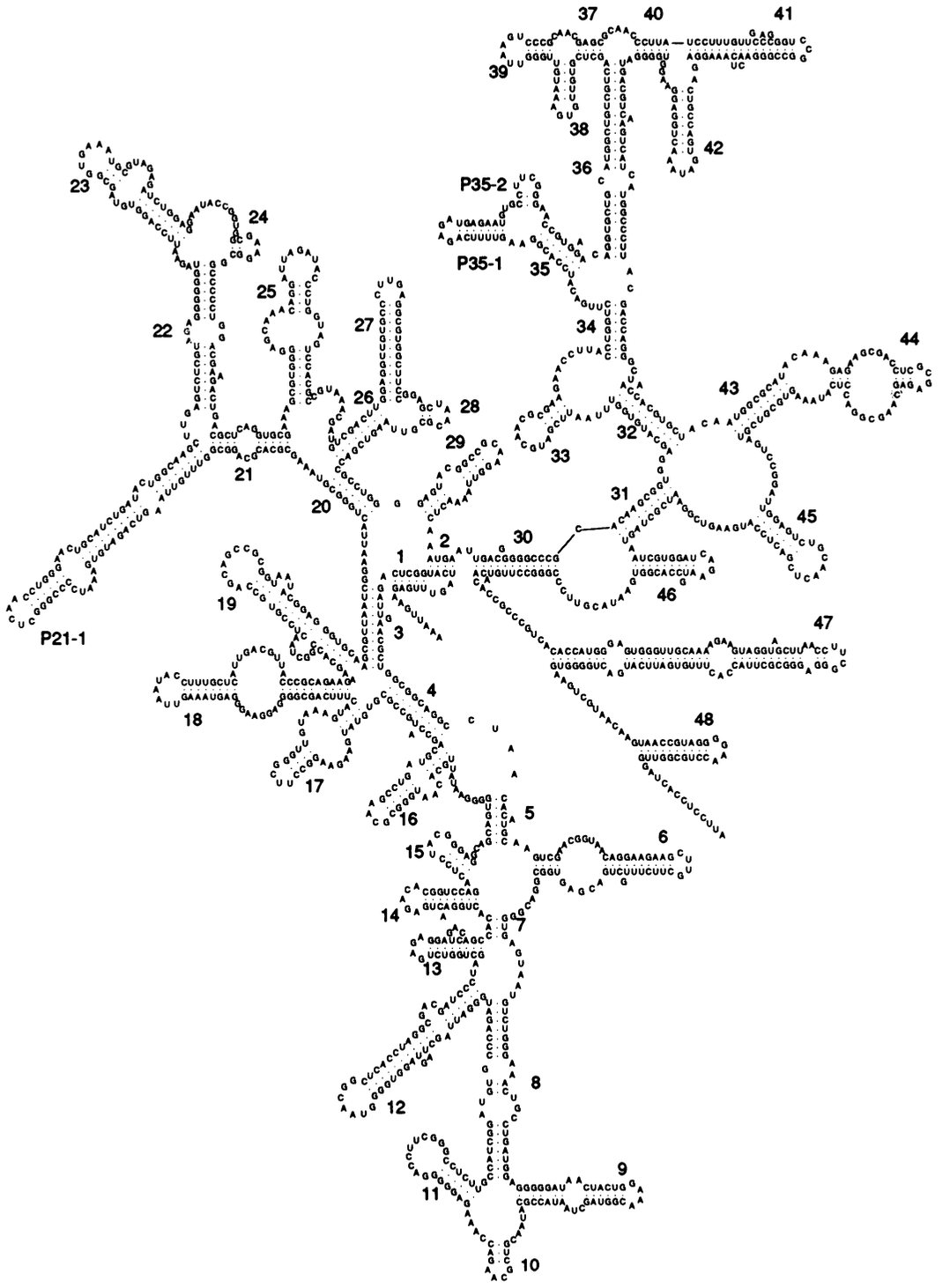
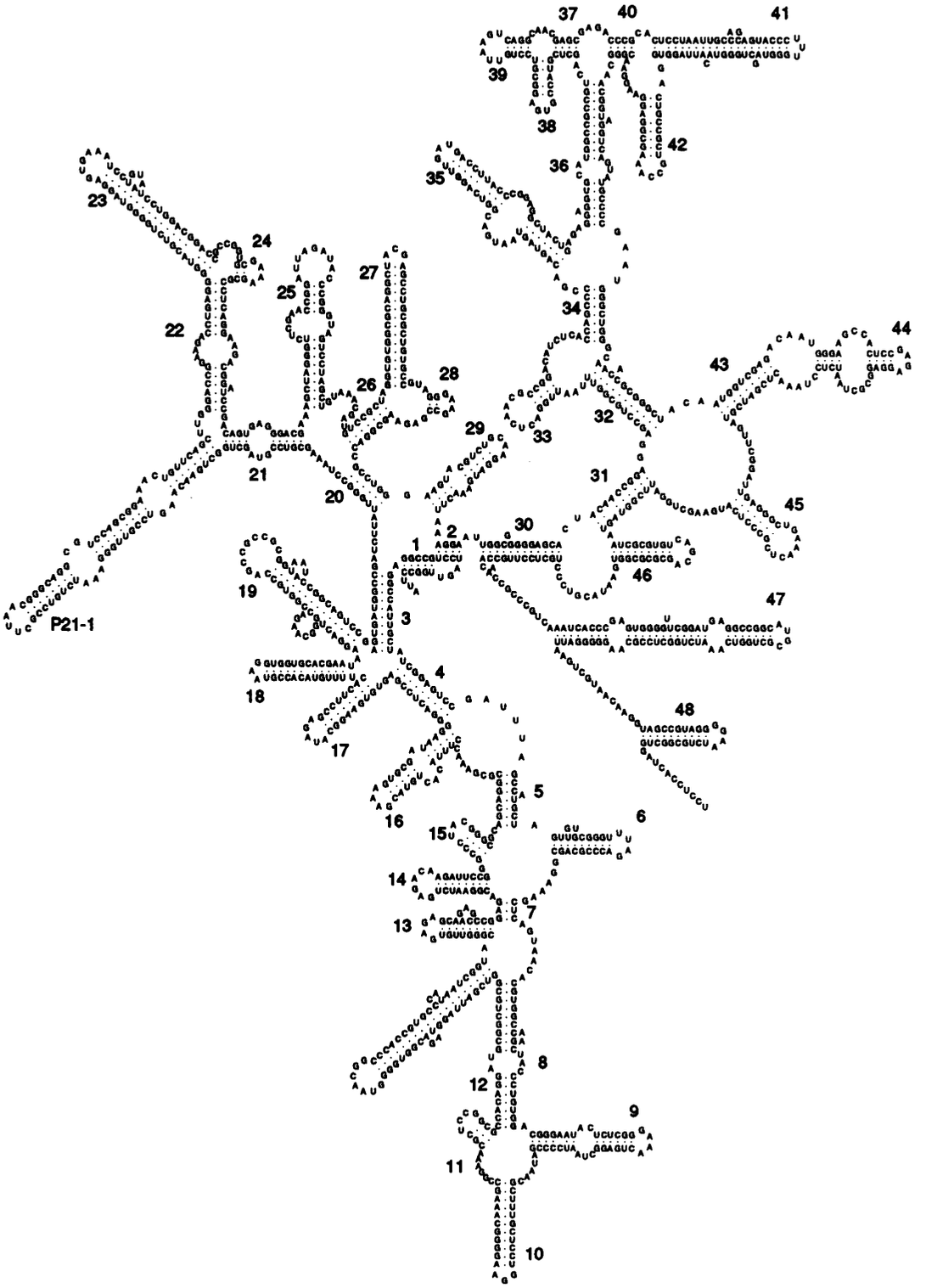
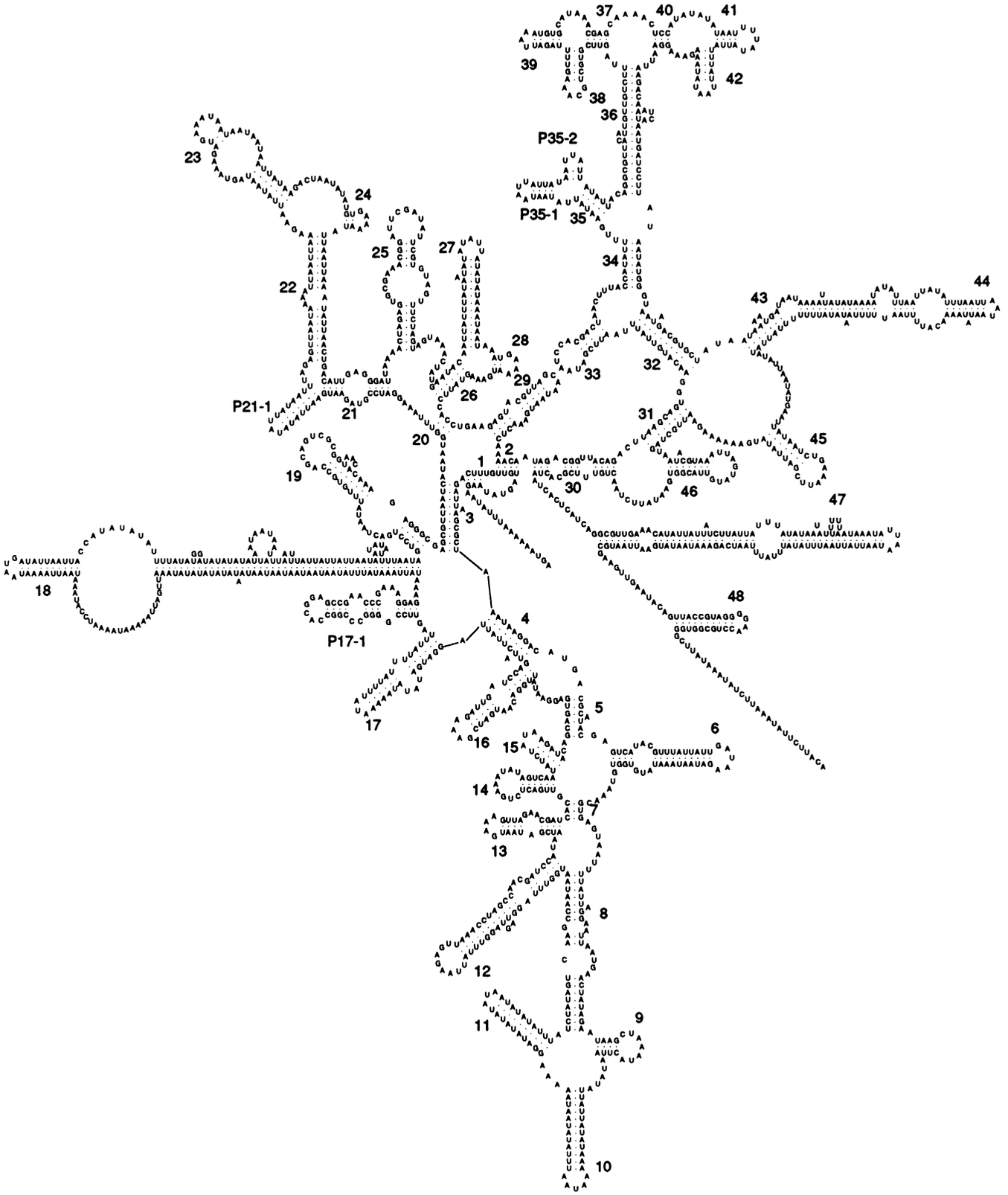


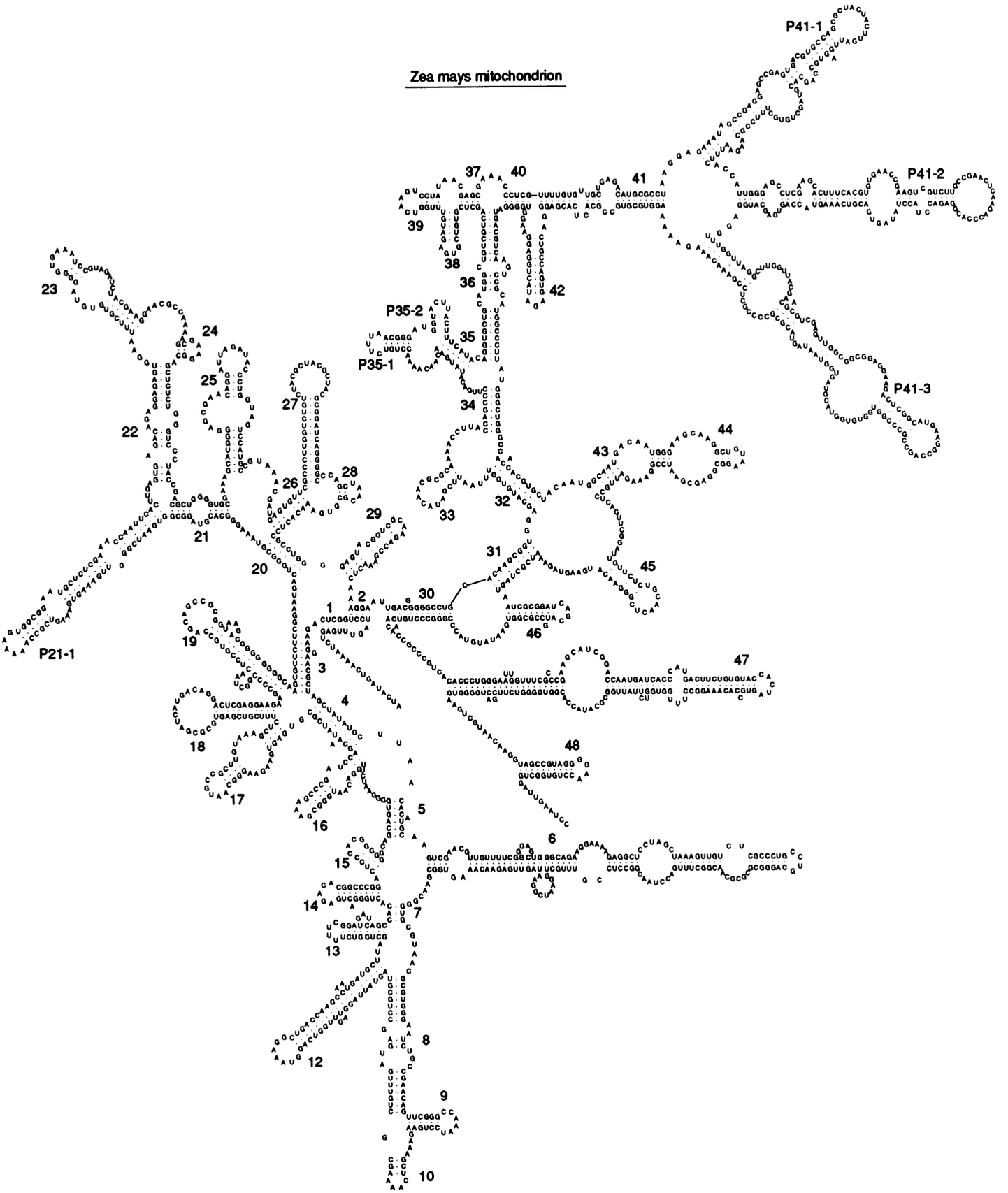
Fig. 4 to 16. Examples of secondary structure models.The model for *Escherichia coli* srRNA (Fig. 4) applies to all eubacterial and plastidial sequences, the model for *Halobacterium cutirubrum* srRNA (Fig. 5) applies to all archaebacterial sequences, and the model for *Saccharomyces cerevisiae* srRNA (Fig. 13) applies to the majority of known eukaryotic sequences. The remaining examples are chosen in order to illustrate a maximum number of structural variants with a minimum number of drawings. Structural variability is especially high among mitochondrial srRNAs, illustrated with sequences from fungal (Fig. 6), plant (Fig. 7), algal (Fig. 8, 9), animal (Fig. 10, 11), and flagellate (Fig. 12) mitochondria. The *Chlamydomonas reinhardtii* mitochondrial srRNA (Fig. 9) consists of 4 discrete segments rather than a single chain (443). The interruptions are situated in helix 6, 17 and 35. The flagellate mitochondrial srRNA model, illustrated with *Trypanosoma brucei* srRNA (Fig. 12) is tentative because alignment with other sequences is especially difficult (see text). Examples of eukaryotic srRNAs with supernumerary helices are those of *Drosophila melanogaster* (Fig. 14) and *Euglena gracilis* (Fig. 15) srRNAs, whereas *Vairimorpha necatrix* srRNA (Fig. 16) misses areas V2 and V4.

Halobacterium cutirubrum



Saccharomyces cerevisiae mitochondrion (no.1)




Zea mays mitochondrion
P41-1
P41-2
P41-3
P35-1
P35-2
P21-1
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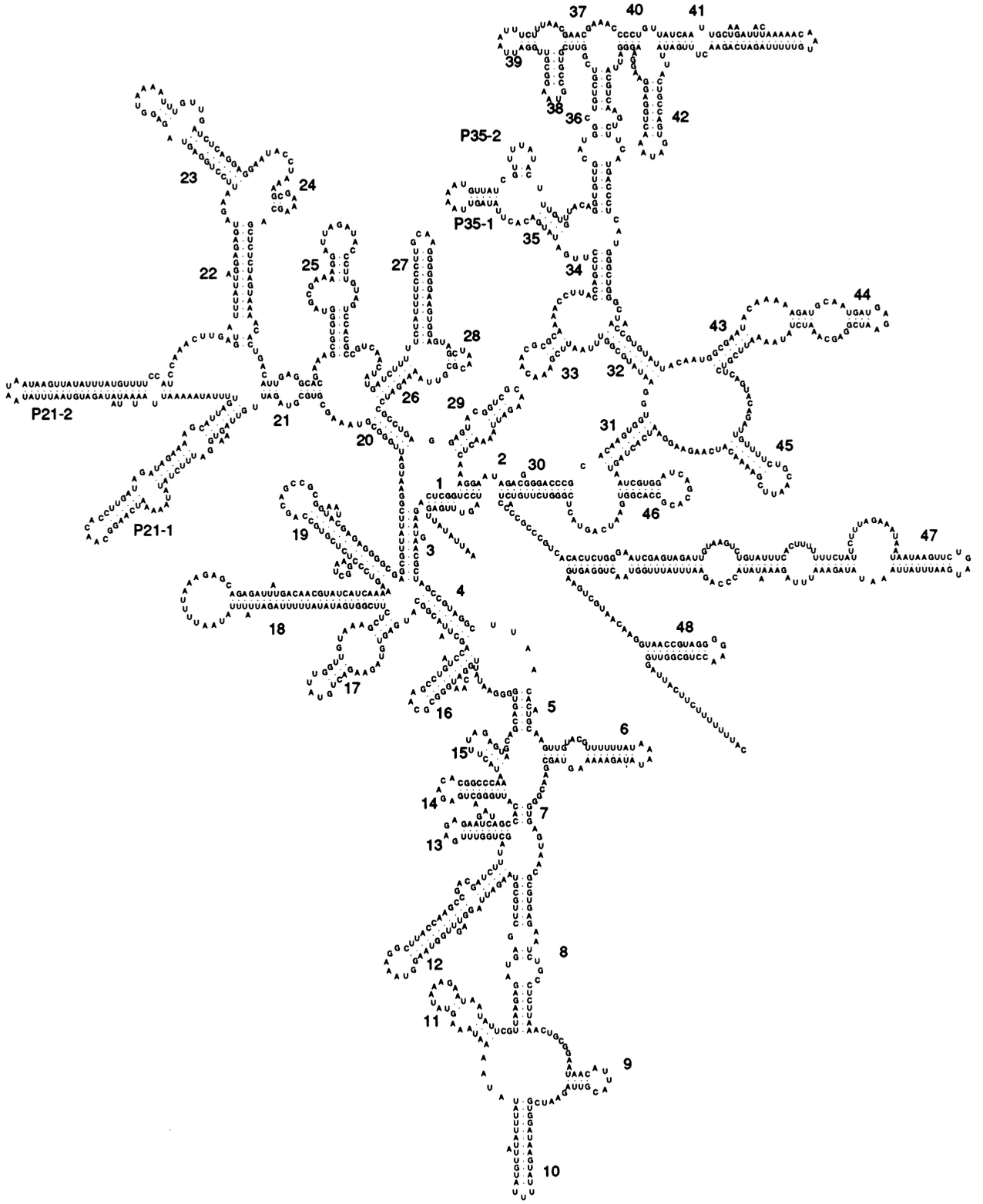
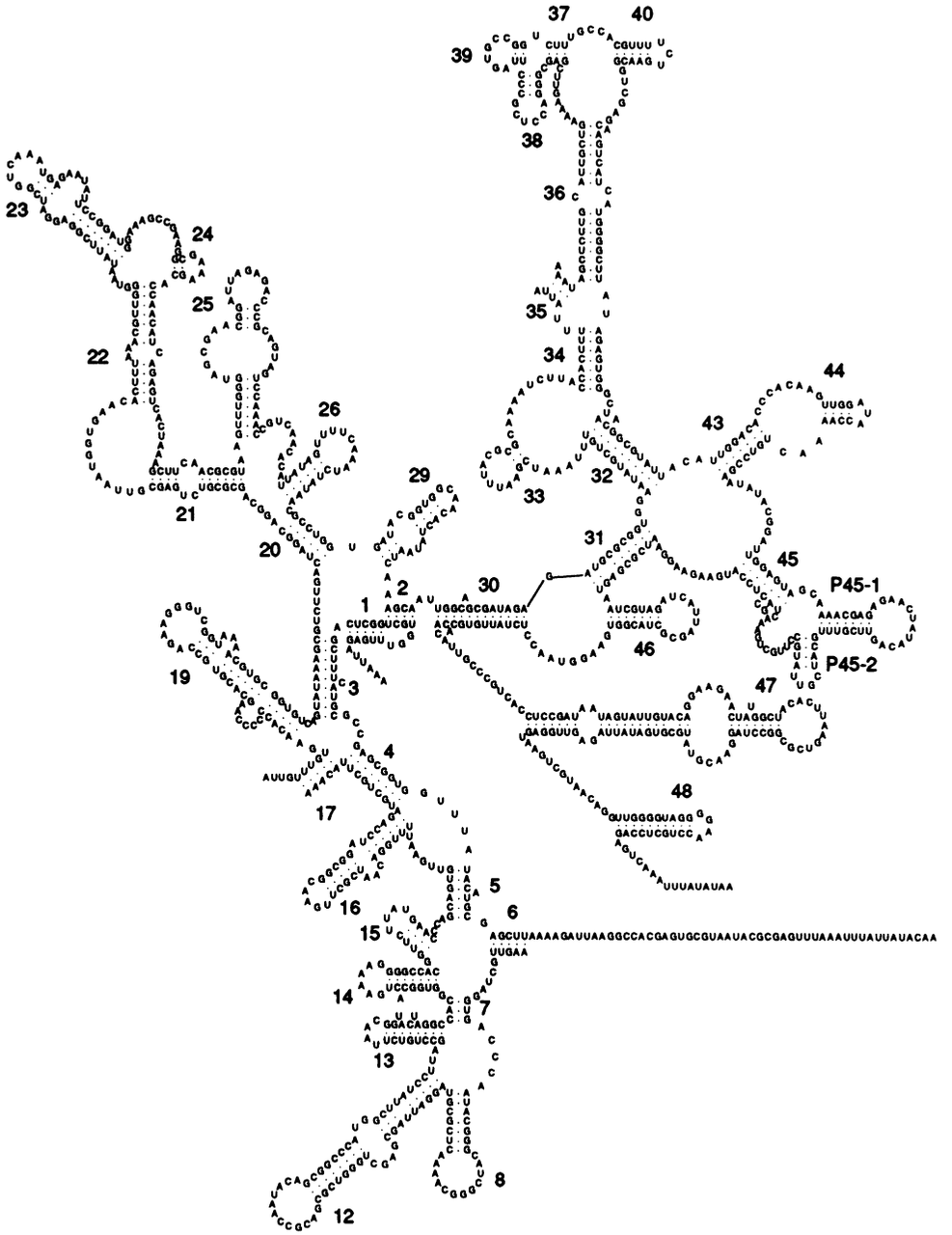
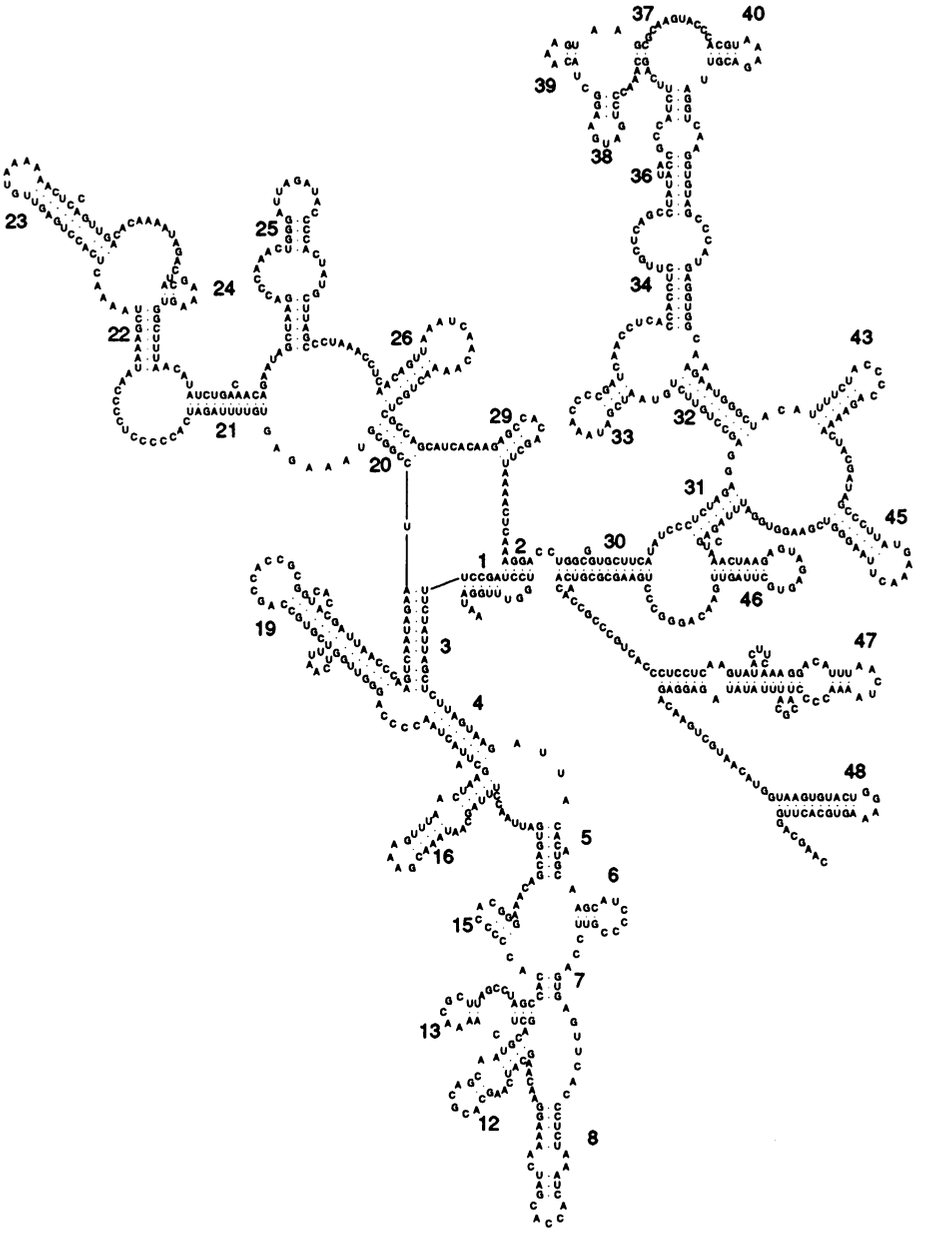
Prototheca wickerhamii mitochondrion



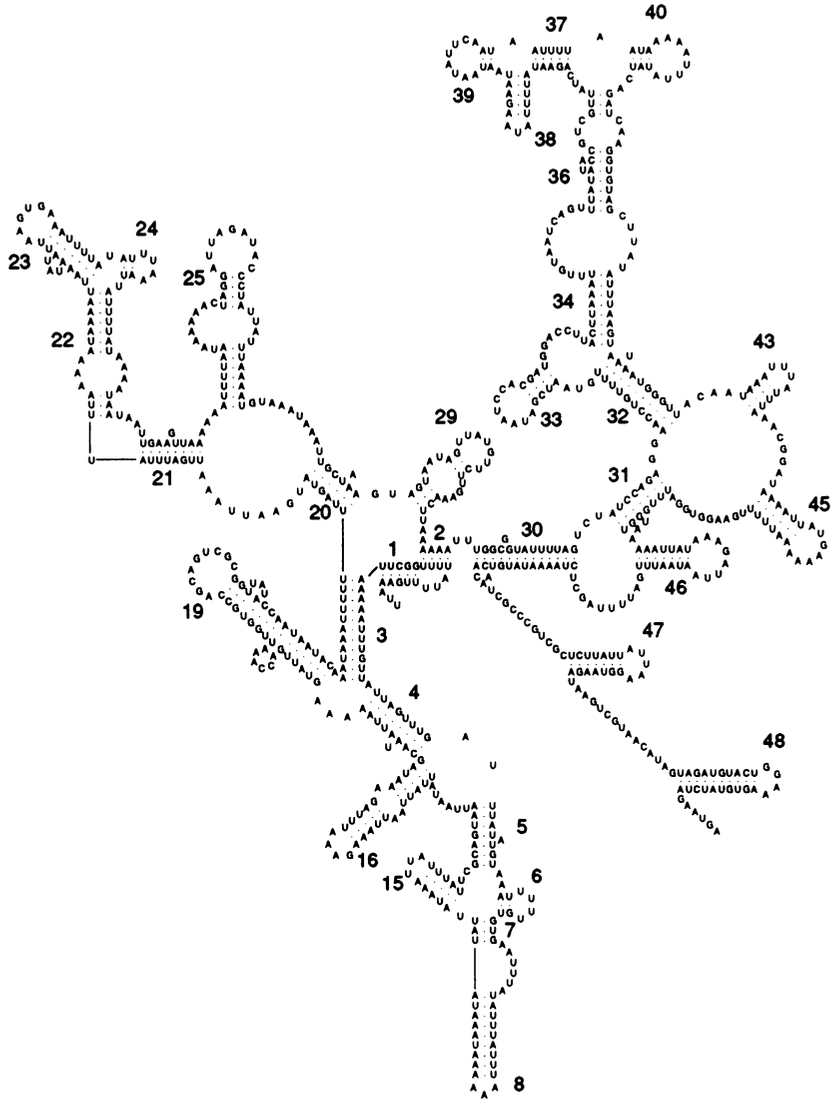
Chlamydomonas reinhardtii mitochondrion



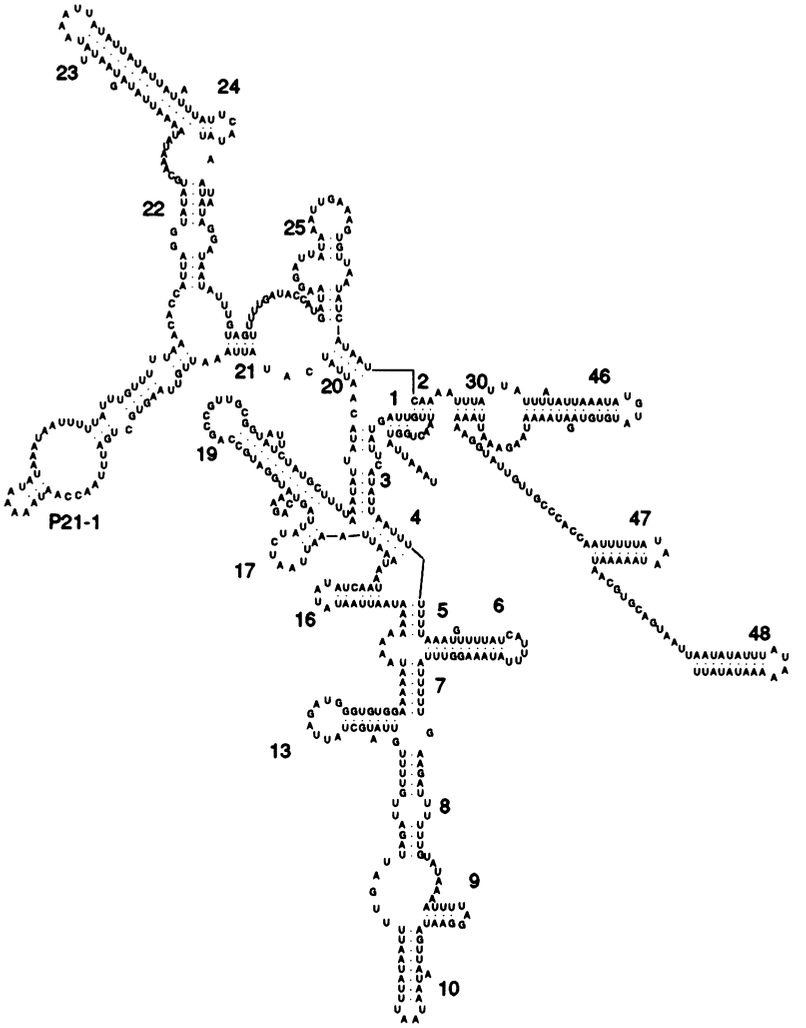
Homo sapiens mitochondrion

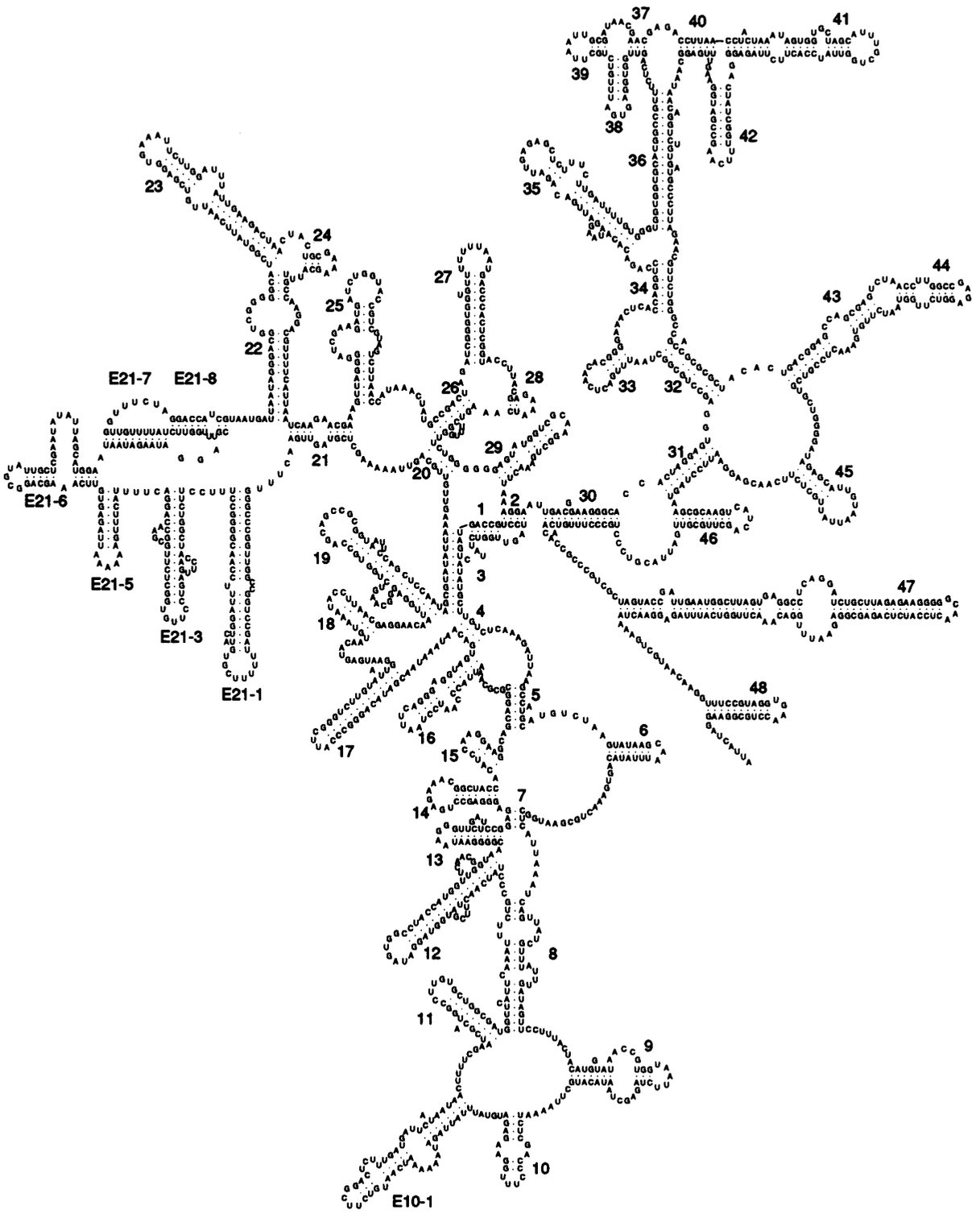


Drosophila yakuba mitochondrion

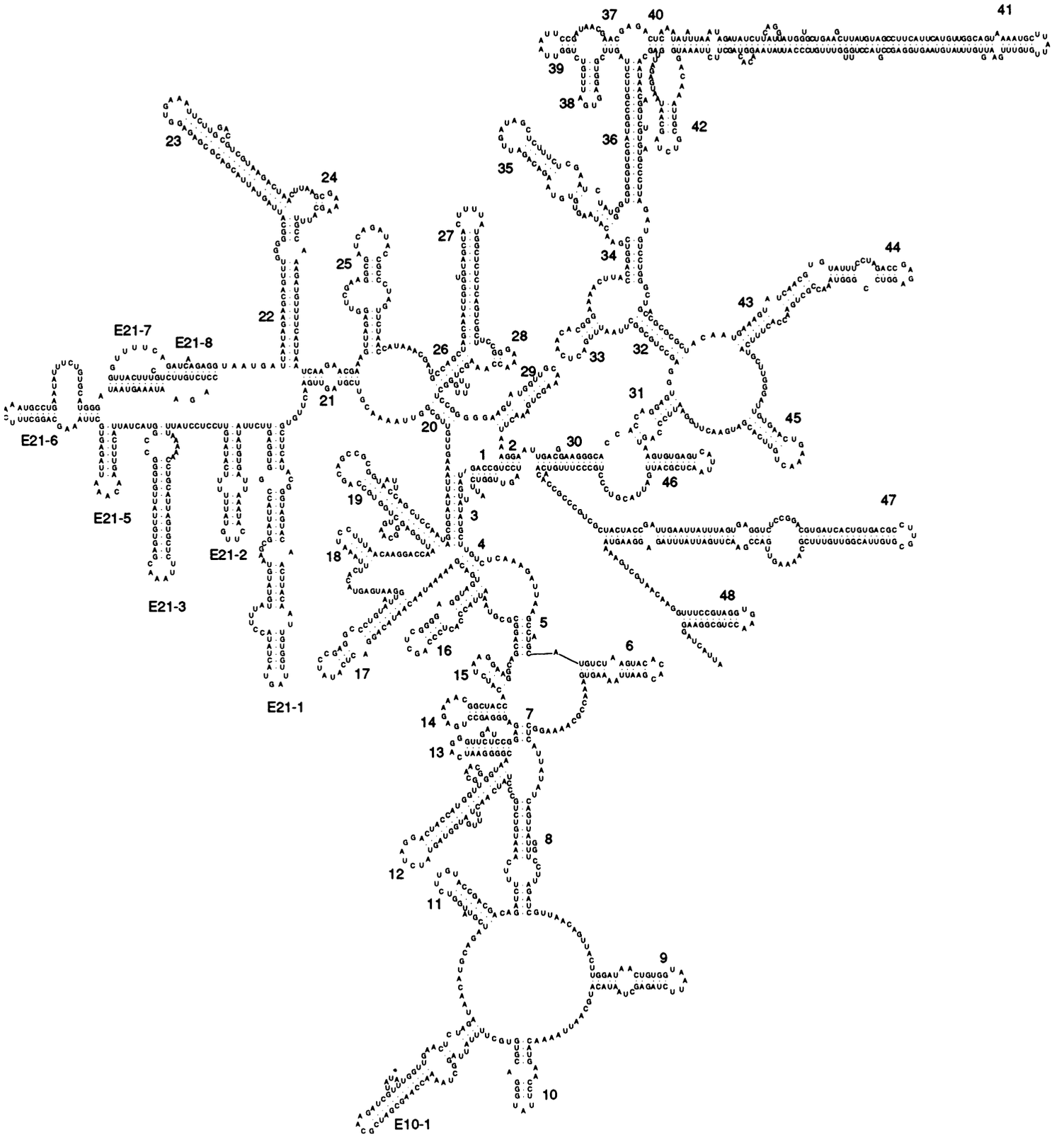


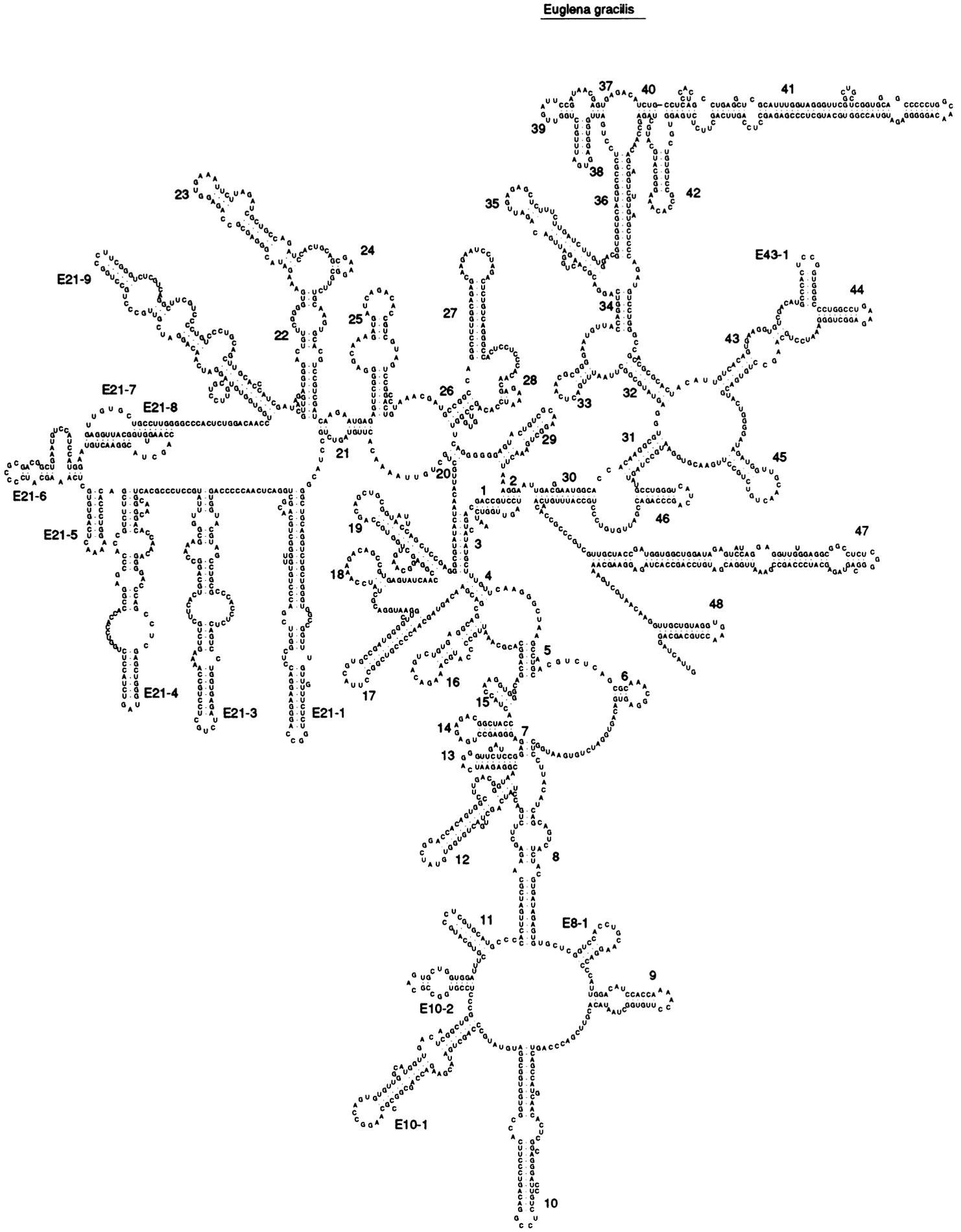
Trypanosoma brucei mitochondrion




Saccharomyces cerevisiae
E21-7
E21-8
E21-6
E21-5
E21-3
E21-1
E10-1

Drosophila melanogaster




Euglena gracilis
E21-9
E21-7
E21-8
E21-6
E21-5
E21-4
E21-3
E21-1
E43-1
E8-1
E10-2
E10-1

Vairimorpha necatrix